

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 18:40:43 ; Search time 8349 Seconds

(without alignments)
7833.055 Million cell updates/sec

Title: US-10-690-617-1

Perfect score: 2190

Sequence: 1 cgcgcggggtgagctcgg.....ctctgtctattcagacgct 2190

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em estba:*
2: em esthum:*
3: em estin:*
4: em estmu:*
5: em estov:*
6: em estpl:*
7: em estro:*
8: em htc:*
9: gb est1:*
10: gb est2:*
11: gb htc:*
12: gb est3:*
13: gb est4:*
14: gb est5:*
15: em estfun:*
16: em estom:*
17: em gss hum:*
18: em gss inv:*
19: em gss pin:*
20: em gss vrt:*
21: em gss fun:*
22: em gss mam:*
23: em gss mus:*
24: em gss pro:*
25: em gss rod:*
26: em gss phg:*
27: em gss vrl:*
28: gb gss1:*
29: gb gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1511.6	69.0	1518	29	AY416154 Homo sapi
2	1225.6	56.0	1518	29	AY416156 Mus muscu
3	1059.8	48.4	1445	29	AY416155 Pan trogl
4	940	42.9	1201	9	AL539375 AL539375

5	928.2	42.4	1034	13	EX401350
6	912.4	41.7	1201	13	EX395129
7	844.2	38.5	972	13	EX459685
8	822.4	37.6	1096	12	BM805189
9	790.8	36.1	2199	11	BC011401
10	786.8	35.9	939	13	BU552890
11	742.4	33.9	880	12	BG705317
12	732	33.4	910	13	BQ932168
13	729.8	33.3	1066	13	BQ277875
14	727	33.2	786	12	BI819446
15	702.4	32.1	896	13	EX328136
16	692.6	31.6	893	12	BG396486
17	688.6	30.5	784	13	BQ571613
18	658.4	30.1	685	12	BG701043
19	639.8	29.2	2508	11	AK031399
20	633.6	28.9	2854	11	AK032070
21	615.2	28.1	749	12	BI756153
22	589.8	26.9	3139	11	AK044660
23	570.6	26.1	727	12	BM950087
24	568.6	26.0	636	12	BI546778
25	556	25.4	1127	13	BU092211
26	529.2	24.2	648	12	BG294573
27	502.6	22.9	589	13	BU671280
28	462.8	21.1	515	12	BM087446
29	445.6	20.3	672	13	BY735290
30	439	20.0	900	12	BI225425
31	435.4	19.9	438	13	EX488903
32	429.8	19.6	841	13	BU115704
33	424.8	19.4	1258	13	BQ067197
34	417	19.0	496	14	CB712914
35	415.6	19.0	589	14	CA751670
36	407.4	18.6	703	28	AQ629789
37	399.4	18.2	1201	9	AL582916
38	397.6	18.2	414	12	BM150448
39	395.4	18.1	915	10	BE562166
40	389.2	17.8	857	13	BU420206
41	385	17.6	746	12	BI687532
42	381.4	17.4	894	13	BU367227
43	371	16.9	503	12	BM951274
44	370.6	16.9	727	12	BM952005
45	370.2	16.9	691	12	BI768851

ALIGNMENTS

RESULT 1	AY416154	1518 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY416154	Homo sapiens CAMKK1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.			
DEFINITION	AY416154	GSS.			
ACCESSION	AY416154.1	GI:39772114			
VERSION	AY416154.1	GSS.			
KEYWORDS	AY416154.1	GSS.			
SOURCE	AY416154.1	Homo sapiens (human)			
ORGANISM	AY416154.1	Homo sapiens			
REFERENCE	AY416154.1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	AY416154.1	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE	AY416154.1	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	AY416154.1	Science 302 (5652), 1960-1963 (2003)			
PUBMED	AY416154.1	14671302			
REFERENCE	AY416154.1	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
AUTHORS	AY416154.1	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE	AY416154.1	Direct Submission			

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>1518
/gene="CAMKK1"
/locus_tag="HCM5796"
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Best Local Similarity 99.7%; Pred. No. 5.2e-290;
Matches 1514; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DB |||||
1 ATGGAGGGGGTCCAGCTGTCTGTGCTCCAGGATCCTCGGCAGAGCTGGTAGACGGGTG 60
QY 233 GCAGCCATCGATGTGACTCACTTGGAGAGGAGATGTCGCCAGAGCCCTACTAGAAAC 292
DB |||||
61 GCAGCCATCGATGTGACTCACTTGGAGAGGAGATGTCGCCAGAGCCCTACTAGAAAC 120
QY 293 GGTGTGACCCGCCACACAGGGGCGAGCTGCTGTGTGATCCCTGGCAGTACTTCAAGA 352
DB |||||
121 GGTGTGACCCGCCACACAGGGGCGAGCTGCTGTGTGATCCCTGGCAGTACTTCAAGA 180
QY 353 CTGCTCCAGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGCA 412
DB |||||
181 CTGCTCCAGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGCA 240
QY 413 GGAAGCTATCTGGAGGCGCAGGCTGGGCTTATGCAAGGAGTGGCAAGGGTGCCTACGGT 472
DB |||||
241 GGAAGCTATCTGGAGGCGCAGGCTGGGCTTATGCAAGGAGTGGCAAGGGTGCCTACGGT 300
QY 473 CCCCGGCTCGCGGAGGCCACCATCGAGTCCACACAGCGGCCATCTCAGATGCGAG 532
DB |||||
301 CCCCGGCTCGCGGAGGCCACCATCGAGTCCACACAGCGGCCATCTCAGATGCGAG 360
QY 533 GACTGCGTGAGCTGAACACAGTCAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT 592
DB |||||
361 GACTGCGTGAGCTGAACACAGTCAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT 420
QY 593 GTGTGAGGCTGGCTCAACAGAAAGTGAAGACAGACACTATGCAATGAAGTCTTTCC 652
DB |||||
421 GTGTGAGGCTGGCTCAACAGAAAGTGAAGACAGACACTATGCAATGAAGTCTTTCC 480
QY 653 AAAAAGAGTTACTGAAGCAGTATGGCTTTCCAGTCCCTCCCGGAGAGGGTCCAG 712
DB |||||
481 AAAAAGAGTTACTGAAGCAGTATGGCTTTCCAGTCCCTCCCGGAGAGGGTCCAG 540
QY 713 GCTGCCAGGAGGACCAAGCAGCTGTGCTCCCTGGAGCGGGTGTACCAAGAGATT 772
DB |||||
541 GCTGCCAGGAGGACCAAGCAGCTGTGCTCCCTGGAGCGGGTGTACCAAGAGATT 600
QY 773 GCCATCTGAAGAGCTGGACCAAGTGAATGTGTGTTCAACTGATCGAGGTCCTGGATGAC 832
DB |||||
601 GCCATCTGAAGAGCTGGACCAAGTGAATGTGTGTTCAACTGATCGAGGTCCTGGATGAC 660
QY 833 CCAGCTGAGGACCACTCTATTGGTGTGTTGACCTCTGAGAAAGGGGCCGTCATGAA 892
DB |||||
661 CCAGCTGAGGACCACTCTATTGGTGTGTTGACCTCTGAGAAAGGGGCCGTCATGAA 720
QY 893 GTGCCCTGTGAAGCCCTTCTCGGAGGAGCAAGCTCGCTCTACCTTGGCGGAGTCAATC 952
DB |||||
721 GTGCCCTGTGAAGCCCTTCTCGGAGGAGCAAGCTCGCTCTACCTTGGCGGAGTCAATC 780
QY 953 CTGGGCTCTGAGTACTTGCATGCTGCCAGAAAGTCTGCCACAGGACATCAAGCCATCAAC 1012
DB |||||
781 CTGGGCTCTGAGTACTTGCATGCTGCCAGAAAGTCTGCCACAGGACATCAAGCCATCAAC 840

QY 1013 CTGCTCTCTGGGGATGATGGGCACTGTAAGATCGCCGACTTTGGCGTCAGCAACACAGTTT 1072
DB |||||
841 CTGCTCTCTGGGGATGATGGGCACTGTAAGATCGCCGACTTTGGCGTCAGCAACACAGTTT 900
QY 1073 GAGGGGACGAGCTCAGCTGTCCAGCAGCGGGGAAACCCAGACATTCATGGCCCCCGAG 1132
DB |||||
901 GAGGGGAAACGAGCTCAGCTGTCCAGCAACCGCGGAAACCCAGACATTCATGGCCCCCGAG 960
QY 1133 GCCATTTCTGATTCGGCCAGAGCTTCACTGCGGAAGCGCTTGGATGTATGGGCCACTGCG 1192
DB |||||
961 GCCATTTCTGATTCGGCCAGAGCTTCACTGCGGAAGCGCTTGGATGTATGGGCCACTGCG 1020
QY 1193 GTCAGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTTCATCTCGGCC 1252
DB |||||
1021 GTCAGTTGTACTGCTTTGTCTATGGGAAGTGCCCGTTCATCGACGATTTTCATCTCGGCC 1080
QY 1253 CTCACAGGAAGATCAAGATGAGCCGTGTGTTCTCTGAGGAGCCAGAAATCAGCGAG 1312
DB |||||
1081 CTCACAGGAAGATCAAGATGAGCCGTGTGTTCTCTGAGGAGCCAGAAATCAGCGAG 1140
QY 1313 GAGCTCAAGGACCTGATCCTGAAGATGTTAGCAAGAAATCCCGAGACGAGAAATGGGGTG 1372
DB |||||
1141 GAGCTCAAGGACCTGATCCTGAAGATGTTAGCAAGAAATCCCGAGACGAGAAATGGGGTG 1200
QY 1373 CCACACATCAAGTTGCACCTTGGTGACCAAGAAACGGGGAGGAGCCCTCTCTCTCGGAG 1432
DB |||||
1201 CCACACATCAAGTTGCACCTTGGTGACCAAGAAACGGGGAGGAGCCCTCTCTCTCGGAG 1260
QY 1433 GAGGAGCACTGACGCTGGTGAGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTC 1492
DB |||||
1261 GAGGAGCACTGACGCTGGTGAGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTC 1320
QY 1493 ATCCCCAGCTGGACCAAGCTGATCCTGTGAAGTCCATGTGTGAGGAAGCGTTCTCTTTGG 1552
DB |||||
1321 ATCCCCAGCTGGACCAAGCTGATCCTGTGAAGTCCATGTGTGAGGAAGCGTTCTCTTTGG 1380
QY 1553 AACCCGTTTGAGCCCGGAGGACGAGGAGGAGGATTCATGTCTGTCTCAGGAACCTA 1612
DB |||||
1381 AACCCGTTTGAGCCCGGAGGACGAGGAGGAGGATTCATGTCTGTCTCAGGAACCTA 1440
QY 1613 CTGTGAAAGAAAGGTTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGAA 1672
DB |||||
1441 CTGTGAAAGAAAGGTTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGAA 1500
QY 1673 GACGAGGCTGCATCCTGA 1690
DB |||||
1501 GACGAGGCTGCATCCTGA 1518
RESULT 2
AY416156
LOCUS
DEFINITION Mus musculus CAMKK1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416156
VERSION AY416156.1 GI:39772116
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1518)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1518)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

<p>Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment. Location/Qualifiers source 1..1518 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>1518 /gene="CAMKK1" /locus_tag="HCM5796"</p>									
<p>Query Match 56.0%; Score 1225.6; DB 29; Length 1518; Best Local Similarity 87.4%; Pred. No. 4.3e-233; Matches 1327; Conservative 0; Mismatches 191; Indels 0; Gaps 0;</p>									
QY	173	ATGAGGGGCTCCAGCTGTCTGCTGCCAGATCTCGGCAGAGCTGTTAGACGGGTG	232						
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QY	233	GCAGCCATCGATGTGACTCACTTGGAGGAGCAGATGGTGCACAGCCCTACTAGAAAC	292						
DB	61	CGGCCATCAATGTGGCCCACTTGGAAAGCAGATGAGGTCCAGAGCCTGCCAGGAT	120						
QY	293	GGTGTGACCCCCACACACGGCCAGAGCTGGCTCTGTGATCCCTGGCAGTACTTCAAG	352						
DB	121	GGTGTGATCTCCACCOCGGCCAGAGCTGCCTCCGTGATCTCTGGCAGTGTCTTCAAG	180						
QY	353	CTGCTCCAGCCGCTAGCCTCTCAGCAGGAGCTTCCCTACAGAGGGGCCAGCA	412						
DB	181	CCCACTCCAGTGCGCCCCAGCCTCTCGCTAGAAAGTTCTCCCTCAGAGACGACCACT	240						
QY	413	GGAAGCTACTGGAGGCCAGCTGGGCTTATGCCAGCGGCGCTGCCAGGCATCTCC	472						
DB	241	GGAAGCTCTTGGGGGCTCAAGTTGGGCTTACTCTACAGGACCTGCCAGTCACTCT	300						
QY	473	CCCOCGGCTCGCGGAGGCCACCATCGAGTCCCAACACGTGGGCCATCTCAGATCGAG	532						
DB	301	CCTCGTCTCGCGGAGACCCACCATCGAGTCCCAACCGTGGCCATCTCAGACACAG	360						
QY	533	GACTGCTGCAGCTCAACCAAGTACAGCTGCAGAGTGAGATTGCAAGGGTGCCTACCGT	592						
DB	361	GACTGTGTGCACACTGAACCAAGTACAGCTGCAGAGTGAGATTGGCAAGGTGCCATGTGT	420						
QY	593	GTGGTGAGCTGGCCCTCAACAGAAAGTGAAGACAGACACTATGCAATGAAAGTCTCTCC	652						
DB	421	GTGGTGAGCTGGCCCTCAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCTCTCC	480						
QY	653	AAAAAGAGTTACTGAAGCAGTATGGCTTTCACGTGGCCCTCCCGAGAGGGTCCCGAC	712						
DB	481	AAAAAGAGTTACTGAAGCAGTATGGCTTTCACGTGGCCCTCCCGAGAGGGTCCCGAC	540						
QY	713	GCTGCCAGGAGGACCCAGCAGCTGCTGCCCCCTGGAGGGGTGTACAGAGATT	772						
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DB	601	GCCATCTTAAGAAGCTGCACCACGTGAATGTAGTCAAAATTGATCGAGTCTCTGATGAT	660						
QY	833	CCAGCTGAGGACAACTCTATTTTGGTGTGTGACCTCTCGAGAAAGGGGCCGCTCATGGAA	892						
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JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 146711302
 REFERENCE 2 (bases 1 to 1445)
 AUTHORS Clark,A.G., Glatowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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 Best Local Similarity 73.6%; Pred. No. 4.1e-200;
 Matches 1064; Conservative 0; Mismatches 381; Indels 0; Gaps 0;
 QY 173 ATGAGGGGGTCCAGCTGCTGCTGCCAGGATCCTGGGCAGAGCTGGTAGACGGGTG 232
 DB 1 ATGAGGGGGTCCAGCTGCTGCTGCCAGGATCCTGGGCAGGCTGGTAGACGGGTG 60
 QY 233 GCAGCCATCATGTGACTCACTTGGAGGAGCAGATGGTGGCCAGAGCCCTACTAGAAC 292
 DB 61 GCAGCCATCATGTGACTCACTTGGAGGAGCAGATGGTGGCCAGAGCCCTACTAGAAC 120
 QY 293 GGTGTGAGACCCCAACAGGGCCAGAGCTGCTGTGTATCCCTGGAGTACTTCAAGA 352
 DB 121 GGTGTGAGACCCCAACAGGGCCAGAGCTGCTGTGTATCCCTGGAGTACTTCAAGA 180
 QY 353 CTGCTCCAGCCCGGCTAGCTCTCAGCCAGGAGCTTTCCCTACAGGAGCGGCCAGCA 412
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 DB 241 GGAAGCTATCTGAGGCGCAGGCTGGCCCTTATGCCACGGGCTGCCAGCCANNNN 300
 QY 473 CCCCGGCTGGCGAGGCCACCATCGAGTCCCAACAGCTGGCCATCTCAGATGCAGAG 532
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 QY 533 GACTGGTGCAGCTGAACCAAGTACAAGCTGCAGAGTGCAGATTGGCAAGGGTGCTACGGT 592
 DB 361 GACTGGTGCAGCTGAACCAAGTACAAGCTGCAGAGTGCAGATTGGCAAGGGTGCTACGGT 420
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 QY 653 AAAAAAGAGTTACTGAAGCAGTATGGCTTCCAGCTGCCCTCCCCGAGAGGGTCCAG 712
 DB 481 AAAAAAGAGTTACTGAAGCAGTATGGCTTCCAGCTGCCCTCCCCGAGAGGGTCCAG 540
 QY 713 GCTGCCAGGAGGAGCAGCAGCAGCTGCTGCCCTGGAGCGGGTGTACAGGAGATT 772
 DB 541 NNN 600
 QY 773 GCATCTGAAGAGCTGACAGGTAATGTGGTCAAACTGATCGAGGTCTTGGATGAC 832
 DB 601 NNN 660
 QY 833 CCAGCTGAGGACAACTTATTGGTGTGGTACCTCTGAGAAAGGGCCCGCTGAGAA 892
 DB 661 NNN 720

QY 893 GTGCCCTGTGACAAAGCCCTTCTCGAGAGAGCAAGCTCGCTTCTACCTCGGAGCACTCATC 952
 DB 721 NNN 780
 QY 953 CTGGGCTCGAGTACTTGCACCTGCGAGAGATCGTCCACAGGAGCATCAAGCCATCCCAAC 1012
 DB 781 NNN 840
 QY 1013 CTGCTCTGGGGATGATGGGCACGTCGAGATCGCCGACTTTGGCGTCAGCAACACAGTTT 1072
 DB 841 CTGCTCTGGGGATGATGGGCACGTCGAGATCGCCGACTTTGGCGTCAGCAACACAGTTT 900
 QY 1073 GAGGGGAACGACGCTCAGCTGTCCAGACGCGGGGAACCCAGCATTCATGGCCCCCGAG 1132
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 DB 1141 GACCTCAAGATCTGATCTCTGAAGATGTAGACAAGATCCGAGACGAGATTTGGGGTG 1200
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 QY 1433 GAGGAGCAGTGCAGCGTGGTGGAGTGCAGAGGGGAGGTTAAGAACTCAGTCAGGCTC 1492
 DB 1261 GAGGAGCAGTGCAGCGTGGTGGAGTGCAGAGGGGAGGTTAAGAACTCAGTCAGGCTC 1320
 QY 1493 ATCCCCAGCTGGACCAAGTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG 1552
 DB 1321 ATCCCCAGCTGGACCAAGTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG 1380
 QY 1553 AACCGTTTGAAGCCCGAGGACGAGGGAAGAGGATCCATGTCTGCTCAGGAAACCTA 1612
 DB 1381 AACCGTTTGAAGCCCGAGGACGAGGGAAGAGGATCCATGTCTGCTCAGGAAACCTA 1440
 QY 1613 CTGGT 1617
 DB 1441 CTGGT 1445

RESULT 4
 AL539375
 LOCUS AL539375 Homo sapiens FETAL BRAIN Homo sapiens cdna clone
 DEFINITION CS0DF033Y017 5-PRIME, mRNA sequence.
 ACCESSION AL539375
 VERSION AL539375.2 GI:31263943
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12868532.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8786.r For
 more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF033AH09QPl&cluster=8786.r)
 cgi-bin/cluster.cgi?seq=CS0DF033AH09QPl&cluster=8786.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DF033AH09QPl.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
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 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 42.9%; Score 940; DB 9; Length 1201;
 Best Local Similarity 97.2%; Pred. No. 2.6e-176;
 Matches 1005; Conservative 5; Mismatches 16; Indels 8; Gaps 5;

QY	178	GGGGGGTTCAGTGTCTGTCAGAGATCTCTCGGCAGAGCTGGTAGAACGGTGGCAGC	237
Db	65	GGGGGGTTCAGTGTCTGTCAGAGATCTCTCGGCAGAGCTGGTAGAACGGTGGCAGC	124
QY	238	CATCATGTGACTACTTGGAGGAGCAGATGCTGCGCCAGAGCTTACTAGAAACGGTGT	297
Db	125	CATCATGTGACTACTTGGAGGAGCAGATGCTGCGCCAGAGCTTACTAGAAACGGTGT	184
QY	298	GGACCCCCCACCACGGGCGCAGAGTGCCTCTGTGATCCCTGGCAGTACTTCAAGACTGT	357
Db	185	GGACCCCCCACCACGGGCGCAGAGTGCCTCTGTGATCCCTGGCAGTACTTCAAGACTGT	244
QY	358	CCAGCCCGGCTAGCTCTCAGCAGGAGGTTTCCCTACAGAGCGGCCAGCAGGAAG	417
Db	245	CCAGCCCGGCTAGCTCTCAGCAGGAGGTTTCCCTACAGAGCGGCCAGCAGGAAG	304
QY	418	CTATCTGGAGGCGAGGCTGGGCTTATGCCACGGGCGCTGCCAGCCATCTCCCCCG	477
Db	305	CTATCTGGAGGCGAGGCTGGGCTTATGCCACGGGCGCTGCCAGCCATCTCCCCCG	364
QY	478	GGCCTGGCGGAGGCGCCACCATCGAGTCCACACAGCTGGCCATCTCAGATGCAGAGACTG	537
Db	365	GGCCTGGCGGAGGCGCCACCATCGAGTCCACACAGCTGGCCATCTCAGATGCAGAGACTG	424
QY	538	CGTGAGCTGAACAGTACAGCTGACAGTGAAGTGGCAGAGGTCCTCAGTGTGTGT	597
Db	425	CGTGAGCTGAACAGTACAGCTGACAGTGAAGTGGCAGAGGTCCTCAGTGTGTGT	484
QY	598	GAGGCTGGCTACACGAAAGTGAACAGACACATATGCAATGAAAGTCTTTCCAAAAA	657
Db	485	GAGGCTGGCTACACGAAAGTGAACAGACACATATGCAATGAAAGTCTTTCCAAAAA	544
QY	658	GAAGTACTGAACAGTATGGCTTTCCAGTTCGCTCCCTCCCGGAGAGGTCCTCAGGCTGC	717
Db	545	GAAGTACTGAACAGTATGGCTTTCCAGTTCGCTCCCTCCCGGAGAGGTCCTCAGGCTGC	604
QY	718	CCAGGAGGACCAAGCAGAGCTGTGCTCCCTGGAGCGGGTGTACAGAGATTGCCAT	777
Db	605	CCAGGAGGACCAAGCAGAGCTGTGCTCCCTGGAGCGGGTGTACAGAGATTGCCAT	654
QY	778	CCTGAGAGCTGGACACAGTGAATGCTGCTCAACTGATCGAGTCTTGATGACCCAGC	837
Db	665	CCTGAGAGCTGGACACAGTGAATGCTGCTCAACTGATCGAGTCTTGATGACCCAGC	724

QY	838	TGAGGACAACTCTATTGTTGTTTACCTCTCTGAGAAAGGGGCCCGTCATGAAAGTGCC	897
Db	725	TGAGGACAACTCTATTGTTGTTTACCTCTCTGAGAAAGGGGCCCGTCATGAAAGTGCC	784
QY	898	CTGTGACAAAGCCCTTCTCGGAGGAGCAGCTGCTTACCTGGGGAGCTCATCTCTGGG	957
Db	785	CTGTGACAAAGCCCTTCTCGGAGGAGCAGCTGCTTACCTGGGGAGCTCATCTCTGGG	844
QY	958	CCTCGAGTACTTGCACCTGCCAGAAAGATCGTCCACAGGAGACATCAAGCCATCCAACTGCT	1017
Db	845	CCTCGAGTACTTGCACCTGCCAGAAAGATCGTCCACAGGAGACATCAAGCCATCCAACTGCT	904
QY	1018	CCTGGGGGATGATGGGCACGTGAGATCGCGACTTTTGGCGTGCAGCAACCGATTGGA--GG	1076
Db	905	CCTGGGGGATGATGGGCACGTGAGATCGCGACTTTTGGCGTGCAGCAACCGATTGGA--GG	964
QY	1077	GGAGGAGCTCAGCTGTCAGGACGGGGGAGCCAGGAGCTTATGATGCCCCCGAGGCA	1136
Db	965	GGAGGAGCTCAGCTGTCAGGACGGGGGAGCCAGGAGCTTATGATGCCCCCGAGGCA	1021
QY	1137	TTTCTGATTCGGGCGCAGAGCTTCTAGTGGGAAAGCCCTTGGATGATGGGCCACTGGCGTCA	1196
Db	1022	TTTCTGATTCGGC--AGAGCTCAGTGGGAGGSCCTTGGATGATGGGC--ACTGGGGYA	1077
QY	1197	CGTTGATCTGCTTT 1210	
Db	1078	CGTTGATCTGHTTK 1091	

RESULT 5
 BX401350
 LOCUS
 DEFINITION
 CDNA clone CS0DK012YG22 5-PRIME, mRNA sequence.
 ACCESSION
 BX401350
 VERSION
 BX401350.1
 GI:30630361
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1. (bases 1 to 1034)
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8786.r For
 more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DK012BD11QPl&cluster=8786.r)
 cgi-bin/cluster.cgi?seq=CS0DK012BD11QPl&cluster=8786.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DK012BD11QPl.

FEATURES
 Location/Qualifiers
 1..1034
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DK012YG22"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoRV
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

QY 910 CTCTCTGGAGGAGCAAG 926
 |||||
 Db 956 CTCTCTGGAGGAGCAAG 972

RESULT 8

BM805189

LOCUS

DEFINITION BM805189 1096 bp mRNA linear EST 05-MAR-2002
 AGENCOURT_6499735 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728398

S, mRNA sequence.

ACCESSION

BM805189

VERSION

BM805189.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1096)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM12724 row: a column: 07

High quality sequence stop: 633.

Location/Qualifiers

1..1096

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5728398"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_124"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: EcoRV

(destroyed); Site 2: NotI; RNA source male hippocampus,

age 27. Library is oligo-dT primed and directionally

cloned (EcoRV site is destroyed upon cloning). Average

insert size 1.4 kb, insert size range 0.9-4 kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 012."

ORIGIN

Query Match

Best Local Similarity

Matches 948; Conservative 0; Mismatches 52; Indels 15; Gaps 8;

QY 130 GTTCCCAACAGGCTACGACAGCAACACCCCTTGACTGAAGCAATGAGGGGTCCAGC 189

Db 35 GTTCCCAACAGGCTACGACAGCAACACCCCTTGACTGAAGCAATGAGGGGTCCAGC 94

QY 190 TGCTGTGTCAGAGATCCTCGGGCAGAGCTGGTAGAACGGGTGCGACCCATCGATGTGAC 249

Db 95 TGCTGTGTCAGAGATCCTCGGGCAGAGCTGGTAGAACGGGTGCGACCCATCGATGTGAC 154

QY 250 TCACCTGGAGGAGCAGATGTTGCCCGCAGAGCTTACTAGAACGGGTGAGACCCCCACC 309

Db 155 TCACCTGGAGGAGCAGATGTTGCCCGCAGAGCTTACTAGAACGGGTGAGACCCCCACC 214

QY 310 ACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCC 369

Db 215 ACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCC 274

QY 370 TAGCCTCTAGCCAGGAGCTTCCCTACAGGAGCGGCCAGAGAGCTATCTGGAGGC 429

Db 275 TAGCCTCTAGCCAGGAGCTTTCCCTACAGAGGGGCCAGCAGCTATCTGGAGGC 334
 QY 430 GCAGGCTGGGCTTTATGCCACGGGGCTTGCCAGCCACATCTCCCTCCGGGGCTTGGCGGAG 489
 |||||
 Db 335 GCAGGCTGGGCTTTATGCCACGGGGCTTGCCAGCCACATCTCCCTCCGGGGCTTGGCGGAG 394
 QY 490 GCCCACCATTGAGTCCACACCGTGGCCATCTCAGATGCAGAGACTGCGTGCAGCTGAA 549
 |||||
 Db 395 GCCCACCATTGAGTCCACACCGTGGCCATCTCAGATGCAGAGACTGCGTGCAGCTGAA 454
 QY 550 CCAGTACAAGCTGCAGAGTGGCAAGGGTGCCTACGGTGTGGTGGAGCTGGCCCTA 609
 |||||
 Db 455 CCAGTACAAGCTGCAGAGTGGCAAGGGTGCCTACGGTGTGGTGGAGCTGGCCCTA 514
 QY 610 CAACGAAGTGAAGACAGACACTATGCAATGAAAGTCTTTTCCAAAAGAGTTACTGAA 669
 |||||
 Db 515 CAACGAAGTGAAGACAGACACTATGCAATGAAAGTCTTTTCCAAAAGAGTTACTGAA 574
 QY 670 GCAGTATGGCTTTCCACGTGCCCTCCCGAGAGGGTCCAGGCTGCCAGGGAGGACC 729
 |||||
 Db 575 GCAGTATGGCTTTCCACGTGCCCTCCCGAGAGGGTCCAGGCTGCCAGGGAGGACC 634
 QY 730 AGCCAAGCAGCTGCTG-CCCTCTGGAGCGGGTGTACACAGAGATGCCATCTCTGAAGAAGC 788
 |||||
 Db 635 AGCCAAGCAGCTGCTGCCCCCTGGAGCGGGTGTACACAGAGATGCCATCTCTGAAGAAGC 694
 QY 789 TGGACACGTTGATGTGGTCAAACTGATGAGGCTCTGGATGACCCAGCTGAGGACCAACC 848
 |||||
 Db 695 TGGACACGTTGATGTGGTCAAACTGATGAGGCTCTGGATGACCCAGCTGAGGACCAACC 754
 QY 849 TCTATTGGG-TGTTTGACCTCTGAGAAAGGGG-CCCGTCTATGGAAGTCCCTGTGACAA 906
 |||||
 Db 755 TCTATTGGGTTTGGACCTCTGAGAAAGGGGCCCCGTATGGAAGTGGCTGTGACAA 814
 QY 907 -GCCCTTCTCGAGGAGCAAGCTCGCTCTACCTGCGGGAGCTCATCC-TGGGGCTCGAG 964
 |||||
 Db 815 GGGCTTCTCGAGGAGCAAGCTCGCTCTACCTGCGGGAGCTCATCTTTGGGCTCGAG 874
 QY 965 TACTTGACATGCCAGAGATCGTCCACAGGAGCATCAAGCCATCCAACTGCTCTCTGGGG 1024
 |||||
 Db 875 TACTTGACATGCCAGAGATCGTTCACAGGGACATTAAGCCATTCCTCACTGGTTCCTGGG 934
 QY 1025 -----GATGATGGGACGTGAAGATCCCGACTTTTGGCGTCAGCAACC--AGTTTGAAGG 1077
 |||||
 Db 935 GGGATGATGGGGACCTGGAAGATCGCCCACTTTGGGGGCCACCAACCCANTTTGAAGG 994
 QY 1078 GAACGAGCTCAGCTGTTC---AGCAGCGGGGAAACCCAGCATTCATGCCCCC 1129
 |||||
 Db 995 GAACCAAGCTCAACTGTTCCAGAAAGGGGGGAAACCCCAACCATTTCTGGGGCCCC 1049

RESULT 9

BC011401

LOCUS

DEFINITION

BC011401 2199 bp mRNA linear HTC 19-NOV-2003
 Homo sapiens calcium/calmodulin-dependent protein kinase kinase 1,
 alpha, mRNA (cDNA clone IMAGE:387393), with apparent retained
 intron.

ACCESSION

BC011401

VERSION

BC011401.1

KEYWORDS

HTC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2199)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Utsdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krywinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2199)

Strausberg, R.

Direct Submission

Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: ang@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegue, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 13 Row: n Column: 11

This clone has the following problem: retained intron.

FEATURES

source

1. .2199

/organism="Homo sapiens"

/mol_type="mrna"

/db_xref="taxon:9606"

/clone="IMAGE:3873973"

/tissue_type="Eye, retinoblastoma"

/clone_lib="NIH_MGC_67"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 36.1%; Score 790.8; DB 11; Length 2199;

Best Local Similarity 99.7%; Pred. No. 1.7e-146;

Matches 792; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1397 GTGACCAAGACGGGAGGAGGCGCCCTTCTTCGGAGGAGGAGCACTGCGAGCGTGGTGAG 1456

Db 1 GTGACCAAGACGGGAGGAGGCGCCCTTCTTCGGAGGAGGAGCACTGCGAGCGTGGTGAG 60

QY 1457 GTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCAGCTGAGACCAAGGATGTC 1516

Db 61 GTGACAGAGGAGGAGGTTAAGAACTCAGTCAGGCTCATCCAGCTGAGACCAAGGATGTC 120

QY 1517 CTGGTGAAGTCCATGCTGAGGAGCGTCTCTTTGGAAACCGTTTTCAGCCCGGACCGG 1576

Db 121 CTGGTGAAGTCCATGCTGAGGAGCGTCTCTTTGGAAACCGTTTTCAGCCCGGACCGG 180

QY 1577 AGGGAAGAGCGATCCATGCTGCTCCAGGAACCTACTGCTGAAGAAAGGGTTTGGTGAA 1636

Db 181 AGGGAAGAGCGATCCATGCTGCTCCAGGAACCTACTGCTGAAGAAAGGGTTTGGTGAA 240

QY 1637 GGGGGCAAGAGCCCGAGAGCTCCCGGCGTCCAGGAAGACGAGGCTGCATCTTGAGCCCT 1696

Db 241 GGGGGCAAGAGCCCGAGAGCTCCCGGCGTCCAGGAAGACGAGGCTGCATCTTGAGCCCT 300

QY 1697 GCATGCACCCAGGGCCACCCGCGAGCAGACACTCATCCGCGCTCCAGAGGCCCCACCCCTC 1756

Db 301 GCATGCACCCAGGGCCACCCGCGAGCAGACACTCATCCGCGCTCCAGAGGCCCCACCCCTC 360

QY 1757 ATGCAACAGCCGCCCGCGAGGAGGCTGGGGACTCGAGCCCGCTCCAGCCCGCTCC 1816

Db 361 ATGCAACAGCCGCCCGCGAGGAGGCTGGGGACTCGAGCCCGCTCCAGCCCGCTCC 420

QY 1817 CCATCGTGTGATGATGACTCCACGCAACGCACTCCAGGAGCAGACTTGAATGTATGTCA 1876

Db 421 CCATCGTGTGATGATGACTCCACGCAACGCACTCCAGGAGCAGACTTGAATGTATGTCA 480

QY 1877 TTTGGGGTCTTGGGGGAGGGCTCCACAGAGGCCATCTCTCTCTTCTTGGCCCTCTTGG 1936

Db 481 TTTGGGGTCTTGGGGGAGGGCTCCACAGAGGCCATCTCTCTCTTCTTGGCCCTCTTGG 540

QY 1937 CCTGACCCATTCTGTGGGGAAAACCGGGTGCCTCATGGAGCTCAGAAATGCCACCCGGCTG 1996

Db 541 CCTGACCCATTCTGTGGGGAAAACCGGGTGCCTCATGGAGCTCAGAAATGCCACCCGGCTG 600

QY 1997 GTTGGCATGGCTTGGGGCAGAGGAGGAGGAGGAGCAGCAAGATGGAGTGGAGGCCAG 2056

Db 601 GTTGGCATGGCTTGGGGCAGAGGAGGAGGAGGAGGAGCAGCAAGATGGAGTGGAGGCCAG 660

QY 2057 GCTTACCAACAGGAGAGACCTCCCGCTGGGGCGGGGAGGAGGAGTGGTTCAGTGGCACA 2116

Db 661 GCTTACCAACAGGAGAGACCTCCCGCTGGGGCGGGGAGGAGGAGTGGTTCAGTGGCACA 720

QY 2117 GGCATATGTGTGAGAGGGGGGTACCTGCGCCACCTTGGGGTGGTGCCACAGAGCTCTTG 2176

Db 721 GGCATATGTGTGAGAGGGGGGTACCTGCGCCACCTTGGGGTGGTGCCACAGAGCTCTTG 780

QY 2177 TCTATTGACAGCGT 2190

Db 781 TCTATTGACAGCGT 794

RESULT 10

BU552890

LOCUS

DEFINITION AGENCOURT 10373297 NIH MGC 109 Homo sapiens cDNA clone

IMAGE:6576737 5', mRNA sequence.

ACCESSION BU552890

VERSION BU552890.1 GI:22903162

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 939)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLCM2775 row: 1 column: 17

High quality sequence stop: 659.

Location/Qualifiers

1. .939

/organism="Homo sapiens"

/mol_type="mrna"

/db_xref="taxon:9606"

FEATURES

source

Db	184	CAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGCAGGAAGCTATCTGAGGCGCAGCGTG	243
QY	438	GGCCTTATGCCAGGGGCTCGCAGCCACATCTCCCCCGGGGCTGGCGAGGCGCCACCA	497
Db	244	GGCCTTATGCCAGGGGCTCGCAGCCACATCTCCCCCGGGGCTGGCGAGGCGCCACCA	303
QY	498	TCAGTCCCAACACGTCGGGCATCTCAGATGCGAGGAGCTCGCTGCAAGCAACAGTACA	557
Db	304	TCAGTCCCAACACGTCGGGCATCTCAGATGCGAGGAGCTCGCTGCAAGCAACAGTACA	363
QY	558	AGCTGCAGAGTGAGATTGGCGAGGGTGCCTACGCTGTGTGAGGCTGGCTACAGGAA	617
Db	364	AGCTGCAGAGTGAGATTGGCGAGGGTGCCTACGCTGTGTGAGGCTGGCTACAGGAA	423
QY	618	GTGAACACAGACACTATGCAATGAAAGTCTCTTCCAAAAGAAAGTACTGAAGCAGTATG	677
Db	424	GTGAACACAGACACTATGCAATGAAAGTCTCTTCCAAAAGAAAGTACTGAAGCAGTATG	483
QY	678	GCTTTCCAGCTGCGCCCTCCCGGAGAGGGTCCAGGCTGCCAGGAGGACCAAGCAAGC	737
Db	484	GCTTTCCAGCTGCGCCCTCCCGGAGAGGGTCCAGGCTGCCAGGAGGACCAAGCAAGC	543
QY	738	AGCTGCTGCCCTGGAGCGGGTGTACCAGAGATTGCCATCTCTGAAGAGCTGGACCAAG	797
Db	544	AGCTGCTGCCCTGGAGCGGGTGTACCAGAGATTG-CATCTGAAGAGCTGGACCAAG	602
QY	798	TGAATGTGTCTAACTGATCGAGGTCTCTGATGACCCAGCTGAGGACCAACCTCTATTGG	857
Db	603	TGAATGTGTCTAACTGATCGAGGT-CTGATGACCCAGCTGAGGACCAACCTCTATTGG	661
QY	858	TGTTTGACCTCTGAGAAAGGGGCCGTGTATGAAAGTGCCCTGTGACAGGCCCTTCTCGG	917
Db	662	TG-TTGACCTCTGAGAAAGGGG-CGCTCATGGAAGTGCCCTGTGACAGGCCCTTCTCGG	719
QY	918	AGGAGCAAGCTCGCTCTACCTCGGGAGCTCATCTGGGCTCGAGTACTTGCATGCC	977
Db	720	AGGAGCAAGCTCGCTCTACCTCGGGAGCTCATCTGGGCTCGAGTACTTGCATGCC	779
QY	978	AGAA-GATCGTCCACA-GGGACATCAAGCCATCAACCTGCTCTCGGGGATGATGGGCA	1035
Db	780	AGNAGATGTCACAGGGGACCTACGCCATGCAACCTGCTCTGGGGGATGATGGCC	839
QY	1036	CGTGAAGATCGCGACTTTGGCGT 1059	
Db	840	GGTAGCATCGGCAAGTAGCGGT 863	
RESULT 12			
BQ932168			
LOCUS			
DEFINITION			
BQ932168 910 bp mRNA linear EST 21-AUG-2002			
IMAGE:6196986 5', mRNA sequence.			
ACCESSION			
BQ932168			
VERSION			
BQ932168.1 GI:22347199			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 910)			
NIH-MGC http://mgc.nci.nih.gov/ .			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: cgabs-r@mail.nih.gov			
Tissue Procurement: Dr. James R. Lupski			
cDNA Library Preparation: Life Technologies, Inc.			
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)			
Clone distribution: Agencourt Bioscience Corporation			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: LLAMI3606 row: e column: 19			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
High quality sequence stop: 577.			
Location/Qualifiers			
1. .910			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="IMAGE:6196986"			
/sex="male"			
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/dev_stage="adult, 70 yr"			
/lab_host="DH10B"			
/clone_lib="Lupski sciatic nerve"			
/note="Vector: pCMW-SPORT6 (Life Technologies); Site 1:			
NotI; Site 2: SalI; cDNA made by oligo-dT priming.			
Directionally cloned using the following adaptors:			
5'-TCACCCAGCGTCCG-3' and			
5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >			
1 kb for average insert length 1.87 kb. This is a primary			
library, non-amplified. Library constructed by Life			
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor			
College of Medicine) and is available through Life			
Technologies."			
ORIGIN			
Query Match 33.4%; Score 732; DB 13; Length 910;			
Best Local Similarity 94.4%; Pred. No. 5.6e-135;			
Matches 849; Conservative 0; Mismatches 31; Indels 19; Gaps 8;			
QY	272	GGCCAGAGCGCTACTAGAAACGGTGTGACCCGCCACACCGGCGCCAGAGCTGCTCTGTG	331
Db	1	GGCCAGAGCGCTACTAGAAACGGTGTGACCCGCCACACCGGCGCCAGAGCTGCTCTGTG	60
QY	332	ATCCCTGGCAGTACTTCAAGACTGTCTCCAGCGCCGCTAGCCTCTCAGCAGGAAGCTT	391
Db	61	ATCCCTGGCAGTACTTCAAGACTGTCTCCAGCGCCGCTAGCCTCTCAGCAGGAAGCTT	120
QY	392	TCCTACAGAGCGCGCAGCAGAAAGCTATCTGAGGCGCAGCTGGGCTTTATGCCAG	451
Db	121	TCCTACAGAGCGCGCAGCAGAAAGCTATCTGAGGCGCAGCTGGGCTTTATGCCAG	180
QY	452	GGGCTGCGCAGCCACATCTCCCGGGGCTGGCGAGGCGCCACCATCGATCCCAACAC	511
Db	181	GGGCTGCGCAGCCACATCTCCCGGGGCTGGCGAGGCGCCACCATCGATCCCAACAC	240
QY	512	GTGGCCATCTCAGATGCGAGGAGCTCGCTGCAGCTGAACAGTACAAGCTCAGAGTGAG	571
Db	241	GTGGCCATCTCAGATGCGAGGAGCTCGCTGCAGCTGAACAGTACAAGCTCAGAGTGAG	300
QY	572	ATTGGCAAGGTCCTACGGTGTGTGAGGCTGGCCCTACACGAAAGTGAAGCAGACAC	631
Db	301	ATTGGCAAGGTCCTACGGTGTGTGAGGCTGGCCCTACACGAAAGTGAAGCAGACAC	360
QY	632	TATGCAATGAAAGTCTCTTCCAAAAGAAAGTACTGAAGCAGTATGGCTTTCCACGTCG	691
Db	361	TATGCAATGAAAGTCTCTTCCAAAAGAAAGTACTGAAGCAGTATGGCTTTCCACGTCG	420
QY	692	CCTCCCCCGAGAGGGTCCCAGGCTGCCAGGAGGACCCAGCAAGCAGCTGTGCCCTG	751
Db	421	CCTCCCCCGAGAGGGTCCCAGGCTGCCAGGAGGACCCAGCAAGCAGCTGTGCCCTG	480
QY	752	GAGCGGCTGTACAGGAGATTGCCATCTCTGAAGAGCTGGACCAAGTGAATGTGTCAA	811
Db	481	GAGCGGCTGTACAGGAGATTGCCATCTCTGAAGAGCTGGACCAAGTGAATGTGTCAA	540
QY	812	CTGATCGAGTCTCTGATGATCACCAGCTGAGGACCACTTATTTGTTTGTGACCTCTCG	871
Db	541	CTGATCGAGTCTCTGATGATCACCAGCTGAGGACCACTTATTTGTTTGTGACCTCTCG	600
QY	872	AGAAAGGGGCGCGCTCATGGAAGTGGCCCTGTGACAGCCCTTCTCGGAGGAGC-AACTCG	930
Db	601	AGAAAGGGGCGCGCTCATGGAAGTGGCCCTGTGACAGCCCTTCTCGGAGGAGC-AACTCG	660
QY	931	CCTCTACTGCGGGACGTCATCTCTGGGCTCGAGTACTTGTGCACTGCGCAGAGATCGTCCA	990


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Db      661 CCTCTACTGGGGAGCTCATCTCTGGGCTCGAGTACTTGCACATGCCAGAGATCGTCCA 720
Qy      991 CA-GGGACATCAAGCCATCCAACTGTCTCC---TGGGGATGATGGGCACGTGAAGATCG 1046
Db      721 CAGGGGACATCAAGCCATCCAACTGTCTCTCTGGGGGATGATGGGGCACGGTGAAGA 780
Qy      1047 CCGAC-----TTTCGGGTTCAGCAACCAAGTTT---GAGGGAAACGACGCTCAGC-TGTCC 1096
Db      781 TCGCCCGACATTTGGCGTCAGCAACCAAGTTTGAAGGGGGACCGAACGCTCANTTGTGCC 840
Qy      1097 AGCACGGGGGAA---CCCCAGCATTCATGG---CCCCCGAGGCCATTTCTGATTCGGGCC 1151
Db      841 AGCAACGGGGAAACCCCCAGCATTCATGGCCCCCCCCAGGGCCCATTTCTGATTTCCGGC 899

RESULT 13
BQ277875 1066 bp mRNA linear EST 07-MAY-2002
LOCUS AGENCOURT_70481118 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5804754
5', mRNA sequence.
ACCESSION BQ277875
VERSION BQ277875.1 GI:20488083
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1066)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2042 row: n column: 19
High quality sequence stop: 626.
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/clone="IMAGE:5804754"
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/note="Organ: ovary; Vector: pOTB7; Site: 1: EcoRI; Site: 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
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GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Query Match 33.3%; Score 729.8; DB 13; Length 1066;
Best Local Similarity 89.7%; Pred. No. 1.7e-134;
Matches 877; Conservative 0; Mismatches 83; Indels 18; Gaps 8;
Qy 857 GTGTTTGAACCTCTGAGAAAGGGCCCGTCTATGGAAGTGCCTCTGCAAGCCCTTCTCG 916
Db 36 GTGTTTGAACCTCTGAGAAAGGGCCCGTCTATGGAAGTGCCTCTGCAAGCCCTTCTCG 95
Qy 917 GAGGAGCAAGCTCGCCTTACTCTGGGACGTCATCTGGGCTCGAGTACTTGCATGCG 976
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Qy      977 CAGAAGATCTGTCCACAGGACATCAAGCCATCCAACTGTCTCTCTGGGGGATGATGGGCAC 1036
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Qy      1037 GTGAAGATCGCGGACTTTGGCGTTCAGAAACCAAGTTTGAAGGGAACGACGCTCAGCTGTGCC 1096
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Qy      1097 AGCACGGGGGAAACCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCGGGGCAGAGC 1156
Db      276 AGCACGGGGGAAACCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCGGGGCAGAGC 335
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Db      336 TTCAGTGGGAGGCGCTTGGATGATGGCCACTGGCGTCAAGTGTGACTGCTTGTGTCTAT 395
Qy      1217 GGGAAAGTGCCTCATTCATCGACGATTTTCATCTGTGCCCCCTCCACAGGAGATCAAGAATGAG 1276
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Qy      1277 CCGTGTGTTTCTTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAG 1336
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Qy      1337 ATGTTAGACAAAGATCCCGAGACGAGAAATGGGGTGCAGACATCAAGTTGCACCCCTTGG 1396
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Qy      1576 GAGGAAAGAGCGATCCATGTC--TGCTCCAGGAAA--CCTACTCGTGTGAAAGAAGGG--TT 1629
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Db      936 TCCAGAGGGCCACCCCTTAATGGCACAGCCGCCGCCCGCCAGAGGAGGGGGCTTGGGG 995
Qy      1799 CCCCACTCCCGCCCTCC 1816
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DEFINITION mRNA sequence.
ACCESSION BI819446
VERSION BI819446.1 GI:15930996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 786)
 NIH-MGC <http://img.ncbi.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L14M11436 row: d column: 09
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 /clone_lib="NIH MGC 115"
 /note="Organ: pooled brain, lung, testis; Vector:
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 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5175128"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 115"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPOR16; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 33.2%; Score 727; DB 12; Length 786;
 Best Local Similarity 98.4%; Pred. No. 5.2e-134;
 Matches 755; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
 QY 91 CGCGCCCGCGCCAGGACACTGTGCGCGCGCCAGGTTCCCAACAGGCTACGCGAG 150
 DB 1 CGCGCCCGCGCGCGGACACTGTGCGCGCGCCAGGTTCCCAACAGGCTACGCGAG 60
 QY 151 AAGAACCCCTTACTGAAGCAATGAGGGGGTCCAGCTGTCTGCTCCAGCATCTCG 210
 DB 61 AAGAACCCCTTACTGAAGCAATGAGGGGGTCCAGCTGTCTGCTCCAGCATCTCG 120
 QY 211 GGCAGAGCTGTAGACGGGTGGCAGCCATCGATGTGACTCACTTGAGAGGCGAGATGG 270
 DB 121 GGCAGAGCTGTAGAACGGGTGGCAGCCATCGATGTGACTCACTTGAGAGGCGAGATGG 180
 QY 271 TGGCCCGAGAGCTTACTAGAAAAGGTGTGACCCGCCACCCAGGCGAGAGCTGCTCTGT 330
 DB 181 TGGCCCGAGAGCTTACTAGAAAAGGTGTGACCCGCCACCCAGGCGAGAGCTGCTCTGT 240
 QY 331 GATCCCTGGAGTACTTCAAGACTGTCTCCAGCCCGGCTAGCCTTCTAGCCAGGAAGCT 390
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 QY 391 TTCCCTACAGGAGCGGAGGAGCTATCTGAGGGCGAGGCTGGGCGCTTATGCCAC 450
 DB 301 TTCCCTACAGGAGCGGAGGAGCTATCTGAGGGCGAGGCTGGGCGCTTATGCCAC 360
 QY 451 GGGGCGCTGCAGCCACATCTCCCGCGGCTGGCGAGGCCACCATCGAGTCCACCA 510
 DB 361 GGGGCGCTGCAGCCACATCTCCCGCGGCTGGCGAGGCCACCATCGAGTCCACCA 420
 QY 511 CBTGGCCATCTCAGATGCAGAGGACTGCGTGCAGCTGAACAGTCAAGCTGCAGAGTGA 570
 DB 421 CBTGGCCATCTCAGATGCAGAGGACTGCGTGCAGCTGAACAGTCAAGCTGCAGAGTGA 480
 QY 571 GATTGCGAAGGGTGCCTACGGTGTGTGAGGCTGGCTACAACGAAGTGAAGACAGACA 630

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RESULT 15
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 cDNA clone CS0DK012YG22 5-PRIME, mRNA sequence.
 BX328136
 ACCESSION
 VERSION
 BX328136.1 GI:30338689
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8786.r For
 more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAG049ZH12)
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>
 Contact : Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>
 Faraday Avenue, Genoscope sequence ID : CS0BAG049ZH12_CS04704_1.
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="CS0DK012YG22"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 32.1%; Score 702.4; DB 13; Length 896;
 Best Local Similarity 91.9%; Pred. No. 4.3e-129;
 Matches 787; Conservative 0; Mismatches 61; Indels 8; Gaps 4;
 QY 940 GCGGACGCTGATCCCTGGG-CCTCGAGTACTTGTGACTGCCAGAGATCGTCCACAGGACA 998
 Db 14 GAGGAACGCTGATCCCTGGGCGCTCGAGTACTTGTGACTGCCAGAGATCGTCCACAGGACA 73
 QY 999 TCAAGCCATCCCAACTGCTCTCGGGGATGATGGGACGTTGAAGATCGCCGACTTTGGCG 1058

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Db      74  TCAAGCCATCCAACTGCTCCTGGGGATGATGGCAGCTGAAGATCGCCGACTTTGGCG 133
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Qy      1119 TCATGGCCCCCGAGGCCATTTCTGATTCGGCCAGAGCTTCAGTGGGAAGCCCTTGGATG 1178
Db      194  TCATGGCCCCCGAGGCCATTTCTGATTCGGCCAGAGCTTCAGTGGGAAGCCCTTGGATG 253
Qy      1179 TATGGGCACCTGGCGTCACTGTTGCTACTGTTGTCTATGGAAAGTGCCCATTCATCGACG 1238
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Db      314  ATTTTCATCTGGCCCTCCACAGGAAGATCAAGATGAGCCCGTGGTGTTCCTGAGGAGC 373
Qy      1299 CAGAAATCAGCAGGAGCTCAAGACCTGATCCTGAAGATGTTAGACAAGAAATCCCGAGA 1358
Db      374  CAGAAATCAGCAGGAGCTCAAGACCTGATCCTGAAGATGTTAGACAAGAAATCCCGAGA 433
Qy      1359 CGAGAAATGGGGTGCACACATCAAGTTGCACCCCTTGGGTGACCAAGAACCGGGAGGAGC 1418
Db      434  CGAGAAATGGGGTGCACACATCAAGTTGCACCCCTTGGGTGACCAAGAACCGGGAGGAGC 493
Qy      1419 CCCTTCCCTCGGAGGAGGAGCACTGCAGCGTGGTGGAGGTGACAGAGGGGAGGTTAAGA 1478
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Qy      1479 ACTCAGTCAGGCTCATCCCACTGGACACCGGTGATCCTGCTGAAGTCCATGCTGAGGA 1538
Db      554  ACTCAGTCAGGCTCATCCCACTGGACACCGGTGATCCTGCTGAAGTCCATGCTGAGGA 613
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Db      731  CCGGCGTTCAGAGAGACAGGCTGATTCCTGAGCCCTGCTTGCCCCCAGGCCACCCCGG 790
Qy      1719 CAGCACA----CTCATCCGCGCCTCCAGAGGCCCAACCCCTCATGCAACAGCCGCCGCCG 1774
Db      791  GTGGGTAACTTCTATTCCCGCCTTCGGAGGGGCCACCCCTTTTGTCAAAATCCTCTC 850
Qy      1775 CAGCAGGGGGCTGGG 1790
Db      851  CCCCCAAGCACGTGGG 866
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Search completed: July 12, 2004, 01:17:37
Job time : 8355 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 18:44:47 ; Search time 182 Seconds
(without alignments)

6677.706 Million cell updates/sec

Title: US-10-690-617-1

Perfect score: 2190

Sequence: 1 cgcgcggggtgagctcgg.....ctctgtctattcagacgt 2190

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2190	100.0	2190	4	US-09-729-995-1
2	2190	100.0	2190	4	US-10-135-689-1
3	561.4	25.6	29629	4	US-09-729-995-3
4	561.4	25.6	29629	4	US-10-135-689-3
5	142.8	6.5	288	4	US-09-016-434-1008
6	99.4	4.5	236	4	US-09-016-434-809
7	90.4	4.1	1302	1	US-08-913-050A-2
8	90.4	4.1	1302	4	US-09-016-434-1146
9	87	4.0	1466	2	US-08-749-902-2
10	83.8	3.8	2968	4	US-08-685-852-1
11	83.4	3.8	1599	3	US-09-256-465-1
12	83.4	3.8	1599	4	US-09-167-322-3
13	83.4	3.8	1599	4	US-09-023-655-1004
14	82.8	3.8	1257	4	US-09-799-875-15
15	82.8	3.8	1826	4	US-09-799-875-13
16	82.8	3.8	1864	4	US-09-819-607-1
17	82.8	3.8	1975	3	US-08-852-743-1
18	82.8	3.8	1975	3	US-09-185-370-1
19	82.2	3.8	1636	4	US-09-016-434-1433
20	79.4	3.6	2158	4	US-09-765-815-1
21	79.4	3.6	3604	4	US-09-688-188B-27
22	79.4	3.6	3604	4	US-09-291-417D-27
23	78.6	3.6	1940	4	US-09-718-032-1
24	78.6	3.6	1941	3	US-09-082-737-1
25	78.6	3.6	2050	4	US-09-688-188B-28
26	78.6	3.6	2050	4	US-09-291-417D-28
27	78.6	3.6	2806	4	US-09-688-188B-102

28	78.6	3.6	2806	4	US-09-291-417D-102	Sequence 102, Appl
29	76.2	3.5	1282	2	US-08-878-989-12	Sequence 12, Appl
30	76.2	3.5	1282	3	US-09-272-796-12	Sequence 12, Appl
31	76.2	3.5	1282	4	US-09-016-434-953	Sequence 953, Appl
32	76	3.5	2827	4	US-09-554-726A-11	Sequence 11, Appl
33	76	3.5	2827	4	US-09-554-726A-20	Sequence 20, Appl
34	75.4	3.4	2161	2	US-08-712-709-4	Sequence 4, Appl
35	75.4	3.4	2161	3	US-09-111-444-4	Sequence 4, Appl
36	75.4	3.4	2161	3	US-09-541-228-4	Sequence 4, Appl
37	75.2	3.4	1732	4	US-09-430-564-1	Sequence 1, Appl
38	75	3.4	1637	2	US-08-966-316-10	Sequence 10, Appl
39	75	3.4	3561	1	US-08-097-997A-12	Sequence 12, Appl
40	75	3.4	3561	3	US-08-865-574C-12	Sequence 12, Appl
41	75	3.4	3561	3	US-08-946-994-12	Sequence 12, Appl
42	75	3.4	4080	4	US-09-016-434-1353	Sequence 1353, Ap
43	75	3.4	4176	4	US-09-972-800A-17	Sequence 17, Appl
44	75	3.4	4176	4	US-09-023-655-1378	Sequence 1378, Ap
45	74	3.4	2124	3	US-09-198-122-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-729-995-1
; Sequence 1, Application US/09729995
; Patent No. 6426206
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CLO00904
; CURRENT APPLICATION NUMBER: US/09/729,995
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Human
US-09-729-995-1

Query Match	100.0%;	Score	2190;	DB	4;	Length	2190;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	2190;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	CGCCCGGGCTGAGCTCGCGGATCTGGGCCCCAGCGAGCGGTGGGGCGGGGGCGG	60				
Db	1	CGCCCGGGCTGAGCTCGCGGATCTGGGCCCCAGCGAGCGGTGGGGCGGGGGCGG	60				
QY	61	GGCGGGGGCGCGCAGCAGCAGGAGTGGGGCGGGCGCGGCGCAGGACACTGTGCCCC	120				
Db	61	GGCGGGGGCGCGCAGCAGCAGGAGTGGGGCGGGCGCGGCGCAGGACACTGTGCCCC	120				
QY	121	GGCGCCAGGTTCCTCCCAAGGCTACGCAAGAACCCCTTCACTGAAGCAATGAGGG	180				
Db	121	GGCGCCAGGTTCCTCCCAAGGCTACGCAAGAACCCCTTCACTGAAGCAATGAGGG	180				
QY	181	GGGTCCAGTGTGTGTGTCGCGAGATCTCGGGCAGAGCTGTGTAGAACGGGTGGCAGCAT	240				
Db	181	GGGTCCAGTGTGTGTGTCGCGAGATCTCGGGCAGAGCTGTGTAGAACGGGTGGCAGCAT	240				
QY	241	CGATGTGACTCACTTCGAGGAGGCAATGGTGGCCAGAGCCCTACTAGAAAACGGTGTGGA	300				
Db	241	CGATGTGACTCACTTCGAGGAGGCAATGGTGGCCAGAGCCCTACTAGAAAACGGTGTGGA	300				
QY	301	CCCCCACCACCGGGCAGAGTGCCTCTGTGATCTCCCTGGCAGTACTTCAAGACTGTCTCC	360				
Db	301	CCCCCACCACCGGGCAGAGTGCCTCTGTGATCTCCCTGGCAGTACTTCAAGACTGTCTCC	360				
QY	361	AGCCCGGCTAGCTTCTCAGCCAGGAGCTTTCCTTACAGGAGCGCCAGCAGGAGCTA	420				
Db	361	AGCCCGGCTAGCTTCTCAGCCAGGAGCTTTCCTTACAGGAGCGCCAGCAGGAGCTA	420				

Db 361 AGCCCGCCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGAGCGGCCAGAGAGCTA 420
Qy 421 TCTGAGGCGCAGGCTGGGCTTTATGCAACGGGCTGCGCAGCCACATCTCCCCCGGGC 480
Db 421 TCTGAGGCGCAGGCTGGGCTTTATGCAACGGGCTGCGCAGCCACATCTCCCCCGGGC 480
Qy 481 CTGGGAGGCGCCACCATCGAGTCCCAACAGTGGCCATCTCAGATCGAGAGGACTGGT 540
Db 481 CTGGGAGGCGCCACCATCGAGTCCCAACAGTGGCCATCTCAGATCGAGAGGACTGGT 540
Qy 541 GCAGCTGAACCAAGCTGACAGTGAAGTGGCAAGGGTGCCTACGGTGTGGTGAG 600
Db 541 GCAGCTGAACCAAGCTGACAGTGAAGTGGCAAGGGTGCCTACGGTGTGGTGAG 600
Qy 601 GCTGGCCTACAAAGAAAGTGAAGACAGACATATGCAATGAAGTCTTTTCCAAAGAA 660
Db 601 GCTGGCCTACAAAGAAAGTGAAGACAGACATATGCAATGAAGTCTTTTCCAAAGAA 660
Qy 661 GTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCGAGAGGGTCCACGGCTGCCA 720
Db 661 GTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCGAGAGGGTCCACGGCTGCCA 720
Qy 721 GGGAGGACCAAGCAGCTGCTGCCCTGGAGCGGTGTACAGAGATTTGCCATCCT 780
Db 721 GGGAGGACCAAGCAGCTGCTGCCCTGGAGCGGTGTACAGAGATTTGCCATCCT 780
Qy 781 GAAGAAGCTGACCAAGTGAATGTGTGCTCAAACTGANTGAGTCTGTGATGACCAAGCTGA 840
Db 781 GAAGAAGCTGACCAAGTGAATGTGTGCTCAAACTGANTGAGTCTGTGATGACCAAGCTGA 840
Qy 841 GGACAACTCTATTGTGTGTGACCTCTCAGAAAGGGGCCCTCATGGAAGTGCCTG 900
Db 841 GGACAACTCTATTGTGTGTGACCTCTCAGAAAGGGGCCCTCATGGAAGTGCCTG 900
Qy 901 TGACAAGCCTTCTCGAGGAGCAAGCTCGCTCTACCTCGGGAACGTCATCTCGGGCT 960
Db 901 TGAACAAGCCTTCTCGAGGAGCAAGCTCGCTCTACCTCGGGAACGTCATCTCGGGCT 960
Qy 961 CGAGTACTGCACTGCCAAGATGCTCCACAGGACATCAAGCCATCCACCTGCTCCT 1020
Db 961 CGAGTACTGCACTGCCAAGATGCTCCACAGGACATCAAGCCATCCACCTGCTCCT 1020
Qy 1021 GGGGGATGATGGGCACGTGAAGATCGCGACTTTGGCGTCAGCAACACAGTTTGAAGGGAA 1080
Db 1021 GGGGGATGATGGGCACGTGAAGATCGCGACTTTGGCGTCAGCAACACAGTTTGAAGGGAA 1080
Qy 1081 CGACGCTCAGCTGTCCAGCAACGGCGGAAACCCAGCATTCATGCCCCCGAGGCAATTC 1140
Db 1081 CGACGCTCAGCTGTCCAGCAACGGCGGAAACCCAGCATTCATGCCCCCGAGGCAATTC 1140
Qy 1141 TGATTCGGCCAGAGCTTCAGTGGAGGGCCCTTGGATGTATGGGCCACTGGCGTCACTT 1200
Db 1141 TGATTCGGCCAGAGCTTCAGTGGAGGGCCCTTGGATGTATGGGCCACTGGCGTCACTT 1200
Qy 1201 GTACTGCTTGTCTATGGGAAGTGCCTTTCATCGACGATTTCTCTGGCCCTCCACAG 1260
Db 1201 GTACTGCTTGTCTATGGGAAGTGCCTTTCATCGACGATTTCTCTGGCCCTCCACAG 1260
Qy 1261 GAAGATCAAGATGAGCCGCTGGTGTCTCTGAGAGCCAGAAATCAGCGAGGAGCTCAA 1320
Db 1261 GAAGATCAAGATGAGCCGCTGGTGTCTCTGAGAGCCAGAAATCAGCGAGGAGCTCAA 1320
Qy 1321 GGACTCTGATCTGAAGATGTTAGACAAGAAATCCGAGACGAGAAATGGGGTGGCCAGAT 1380
Db 1321 GGACTCTGATCTGAAGATGTTAGACAAGAAATCCGAGACGAGAAATGGGGTGGCCAGAT 1380
Qy 1381 CAAGTGTGACCCCTTGGGTGACCAAGAAACGGGAGGAGCCCTTCTCTCGAGGAGGAGCA 1440
Db 1381 CAAGTGTGACCCCTTGGGTGACCAAGAAACGGGAGGAGCCCTTCTCTCGAGGAGGAGCA 1440
Qy 1441 CTGACAGCTGTGAGGTGACAGAGGGGAGGTTAAGNACTCAGTCAGGCTCATCCCCAG 1500
Db 1441 CTGACAGCTGTGAGGTGACAGAGGGGAGGTTAAGNACTCAGTCAGGCTCATCCCCAG 1500

Qy 1501 CTGACCAACGGTGAATCTGTGAAGTCCATGCTCAGGAGAGGTTCTTTGGGAACCCGTT 1560
Db 1501 CTGACCAACGGTGAATCTGTGAAGTCCATGCTCAGGAGAGGTTCTTTGGGAACCCGTT 1560
Qy 1561 TGAGCCCCAGCAGCGAGGGAAGAGCGATCCATGCTCTGCTCCAGAAACCTTACTTGGTGAA 1620
Db 1561 TGAGCCCCAGCAGCGAGGGAAGAGCGATCCATGCTCTGCTCCAGAAACCTTACTTGGTGAA 1620
Qy 1621 AGAAGGGTGGTGAAGGGGCAAGAGCCAGAGCTCCCGCGCTCCAGGAAGACGAGGC 1680
Db 1621 AGAAGGGTGGTGAAGGGGCAAGAGCCAGAGCTCCCGCGCTCCAGGAAGACGAGGC 1680
Qy 1681 TGCATCTGAGCCCTGATGACCCAGGGCCACCGGCGACACACTCATCTCCCGGCTC 1740
Db 1681 TGCATCTGAGCCCTGATGACCCAGGGCCACCGGCGACACACTCATCTCCCGGCTC 1740
Qy 1741 CAGAGGCCACCCCTCATGCAACAGCGCCCGCCAGCAGGGGGCTGGGGACTGCAGCC 1800
Db 1741 CAGAGGCCACCCCTCATGCAACAGCGCCCGCCAGCAGGGGGCTGGGGACTGCAGCC 1800
Qy 1801 CCATCCCGGCTTCCCGCATGCTGCTGATGACCTCCACGACGACGTCAGGGAACAG 1860
Db 1801 CCATCCCGGCTTCCCGCATGCTGCTGATGACCTCCACGACGACGTCAGGGAACAG 1860
Qy 1861 ACTGGAATGATGTCATTTGGGGTCTTTGGGGGAGGGCTCCACAGGGCCATCTCTCT 1920
Db 1861 ACTGGAATGATGTCATTTGGGGTCTTTGGGGGAGGGCTCCACAGGGCCATCTCTCT 1920
Qy 1921 TCTTGGGCTCTCTTGGGCTGACCCATTTCTGTGGGGAAACCGGGTGCCTCATGGAGCTCAG 1980
Db 1921 TCTTGGGCTCTCTTGGGCTGACCCATTTCTGTGGGGAAACCGGGTGCCTCATGGAGCTCAG 1980
Qy 1981 AAATGCCACCCGCTGCTTGGCATGCTGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040
Db 1981 AAATGCCACCCGCTGCTTGGCATGCTGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040
Qy 2041 GGCAGGTGGAGGCCAGGCTTACCACACGGAAGAGACTCCCGCTGGGGCCGCGCAGGCC 2100
Db 2041 GGCAGGTGGAGGCCAGGCTTACCACACGGAAGAGACTCCCGCTGGGGCCGCGCAGGCC 2100
Qy 2101 TGGCTCAGCTGSCCAGCAGGATATGTTGGAGAGGGGGTACCTGCCACCTTGGGGTGGT 2160
Db 2101 TGGCTCAGCTGSCCAGCAGGATATGTTGGAGAGGGGGTACCTGCCACCTTGGGGTGGT 2160
Qy 2161 GGCACACAGCTCTTGTCTATTTCAGAGCT 2190
Db 2161 GGCACACAGCTCTTGTCTATTTCAGAGCT 2190

RESULT 2

US-10-135-689-1
; Sequence 1, Application US/10135689
; Patent No. 6670162
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904DIV
; CURRENT APPLICATION NUMBER: US/10135,689
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-135-689-1

[illegible]

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Db 2101 TGGCTCAGTGCACAGGCATATGGTGGAGAGGGGGTACCTGCCACCTTGGGGTGGT 2160
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Qy 2161 GGCACAGAGCTCTTGCTATTCAGAGCT 2190
|||||
Db 2161 GGCACAGAGCTCTTGCTATTCAGAGCT 2190
|||||
RESULT 3
US-09-729-995-3
; Sequence 3, Application US/09729995
; Patent No. 6426206
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000904
; CURRENT APPLICATION NUMBER: US/09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human
US-09-729-995-3

Query Match 25.6%; Score 561.4; DB 4; Length 29629;
Best Local Similarity 96.4%; Pred. No. 1.6e-122;
Matches 585; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
Qy 1585 GCGATCATGCTCTCTCCAGAAACCTACTGTTGTAAGAAGGGTTTGGTGAAGGGGCAA 1644
Db 26526 GAGTCCCTCTGTCTCTCTCCCTGAAACAGGAAAGAGGGTTTGGTGAAGGGGCAA 26585
Qy 1645 GAGCCACAGAGCTCCCGCGCTCCAGGAAGACAGAGCTGCATCTCTGAGCCCTCGATGCAC 1704
Db 26586 GAGCCACAGAGCTCCCGCGCTCCAGGAAGACAGAGCTGCATCTCTGAGCCCTCGATGCAC 26645
Qy 1705 CAGGGGCACCCCGCAGACACTCATCCCGGCTCCAGAGGCCA-CCCTCATGCAAC 1763
Db 26646 CAGGGGCACCCCGCAGACACTCATCCCGGCTCCAGAGGCCA-CCCTCATGCAAC 26705
Qy 1764 AGCGCCCCCGCAGCGAGGGGCTGGGAGCTGCAGCCCACTCCCGCCCTCCCGCATCG 1823
Db 26706 AGCGCCCCCGCAGCGAGGGGCTGGGAGCTGCAGCCCACTCCCGCCCTCCCGCATCG 26765
Qy 1824 TGCTGCATGACCTCCACGACGACGTCAGGGACAGACTGGAAATGATGTATTTGGGG 1883
Db 26766 TGCTGCATGACCTCCACGACGACGTCAGGGACAGACTGGAAATGATGTATTTGGGG 26825
Qy 1884 TCTTGGGGGAGGGCTCCAGAGGCATCTCTCTCTTTTGGCCCTCTTGGCCTGACC 1943
Db 26826 TCTTGGGGGAGGGCTCCAGAGGCATCTCTCTCTTTTGGACCTCTTGGCCTGACC 26885
Qy 1944 CATTTCTGTGGGAAACCGGCTGCCATGGAGCTTCAGAAATGCCACCGGCTGTGGCA 2003
Db 26886 CATTTCTGTGGGAAACCGGCTGCCATGGAGCTTCAGAAATGCCACCGGCTGTGGCA 26945
Qy 2004 TGGCCTGGGGCAGGAGCAGAGCAGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACC 2063
Db 26946 TGGCCTGGGGCAGGAGCAGAGCAGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACC 27005
Qy 2064 ACAACGAAGAGACTTCCCGCTGGGGCCGGCAGGCTTGGCTCAGCTGCCACAGGCATAT 2123
Db 27006 ACAACGAAGAGACTTCCCGCTGGGGCCGGCAGGCTTGGCTCAGCTGCCACAGGCATAT 27065
Qy 2124 GGTGGAGAGGGGGTACCTCTGCCACCTTGGGGTGGTGGCACACAGAGCTCTTGTCTATTC 2183
Db 27066 GGTGGAGAGGGGGTACCTCTGCCACCTTGGGGTGGTGGCACACAGAGCTCTTGTCTATTC 27125
Qy 2184 AGAGCT 2190

|||||
Db 27126 AGAGCT 27132
|||||
RESULT 4
US-10-135-689-3
; Sequence 3, Application US/10135689
; Patent No. 6670162
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000904DIV
; CURRENT APPLICATION NUMBER: US/10/135,689
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-135-689-3

Query Match 25.6%; Score 561.4; DB 4; Length 29629;
Best Local Similarity 96.4%; Pred. No. 1.6e-122;
Matches 585; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
Qy 1585 GCGATCATGCTCTCTCCAGAAACCTACTGTTGTAAGAAGGGTTTGGTGAAGGGGCAA 1644
Db 26526 GAGTCCCTCTGTCTCTCTCCCTGAAACAGGAAAGAGGGTTTGGTGAAGGGGCAA 26585
Qy 1645 GAGCCACAGAGCTCCCGCGCTCCAGGAAGACAGAGCTGCATCTCTGAGCCCTCGATGCAC 1704
Db 26586 GAGCCACAGAGCTCCCGCGCTCCAGGAAGACAGAGCTGCATCTCTGAGCCCTCGATGCAC 26645
Qy 1705 CAGGGGCACCCCGCAGACACTCATCCCGGCTCCAGAGGCCA-CCCTCATGCAAC 1763
Db 26646 CAGGGGCACCCCGCAGACACTCATCCCGGCTCCAGAGGCCA-CCCTCATGCAAC 26705
Qy 1764 AGCGCCCCCGCAGCGAGGGGCTGGGAGCTGCAGCCCACTCCCGCCCTCCCGCATCG 1823
Db 26706 AGCGCCCCCGCAGCGAGGGGCTGGGAGCTGCAGCCCACTCCCGCCCTCCCGCATCG 26765
Qy 1824 TGCTGCATGACCTCCACGACGACGTCAGGGACAGACTGGAAATGATGTATTTGGGG 1883
Db 26766 TGCTGCATGACCTCCACGACGACGTCAGGGACAGACTGGAAATGATGTATTTGGGG 26825
Qy 1884 TCTTGGGGGAGGGCTCCAGAGGCATCTCTCTCTTTTGGCCCTCTTGGCCTGACC 1943
Db 26826 TCTTGGGGGAGGGCTCCAGAGGCATCTCTCTCTTTTGGACCTCTTGGCCTGACC 26885
Qy 1944 CATTTCTGTGGGAAACCGGCTGCCATGGAGCTTCAGAAATGCCACCGGCTGTGGCA 2003
Db 26886 CATTTCTGTGGGAAACCGGCTGCCATGGAGCTTCAGAAATGCCACCGGCTGTGGCA 26945
Qy 2004 TGGCCTGGGGCAGGAGCAGAGCAGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACC 2063
Db 26946 TGGCCTGGGGCAGGAGCAGAGCAGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACC 27005
Qy 2064 ACAACGAAGAGACTTCCCGCTGGGGCCGGCAGGCTTGGCTCAGCTGCCACAGGCATAT 2123
Db 27006 ACAACGAAGAGACTTCCCGCTGGGGCCGGCAGGCTTGGCTCAGCTGCCACAGGCATAT 27065
Qy 2124 GGTGGAGAGGGGGTACCTCTGCCACCTTGGGGTGGTGGCACACAGAGCTCTTGTCTATTC 2183
Db 27066 GGTGGAGAGGGGGTACCTCTGCCACCTTGGGGTGGTGGCACACAGAGCTCTTGTCTATTC 27125
Qy 2184 AGAGCT 2190


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Db      27126 AGACGCT 27132      |||||
RESULT 5
US-09-016-434-1008
; Sequence 1008, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1008:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT04
; CLONE: 926034
; US-09-016-434-1008

Query Match      6.5%; Score 142.8; DB 4; Length 288;
Best Local Similarity 70.7%; Pred. No. 1.4e-24;
Matches 203; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

QY      644  GTCTTTCCAAAAGAGTTACTGAAGCAGATGATGGCTTTTCCAGTCGCGCTCCCGGAG 703
Db      1  GTGCTGTCCAAAAGAGCTGATCCGCGAGCGGGCTTTCCAGTCGCGCTCCCGGAG 60

QY      704  GGGTCCAGGCTCCAGGAGGACGACGACGAGCTGTCGCTCCCTGGAGGGGTGTAC 763
Db      61  GGACCCGGCGAGCTCCTGGAGGCTGCATCCAGCCAGGGGGCCCAATTGAGCAGGTGTAC 120

QY      764  CAGGAGATTGCCATCTCTGAAGAGCTGGACCAAGTGAATGTGTCAAACTGATCGAGGTC 823
Db      121  CAGGAATTTGCCATCTCTCAGAAGCTGGACCAAGTGAATGTGTGAAGCTGTGGAGGTC 180

QY      824  CTGGATGACCCAGCTCAGGACAACTCTATTGTTGTTGTTGACCTCTCTGAGAAAGGGGCCC 883
Db      181  CTGGATGACCCCAATGAGGACCATCTGTACATGTGTGTGA-ATGGTCAACCAAGGGGCC 239

QY      884  GTCATGGAAGTGCCTGTGTGACAGCCCTTCTCGGAGGAGCAAGCTCG 930

Db      240  GTGATGAAGTGCCTCCACCCCTTAACACCTTTTGTAGACAGGCGCG 286
RESULT 6
US-09-016-434-809
; Sequence 809, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 809:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT03
; CLONE: 531037
; US-09-016-434-809

Query Match      4.5%; Score 99.4; DB 4; Length 236;
Best Local Similarity 71.8%; Pred. No. 2.1e-14;
Matches 155; Conservative 0; Mismatches 59; Indels 2; Gaps 2;

QY      875  AAGGGGCCCGTCATGGAAGTGCCC-TGTGACAAAGCCCTTCTCGGAGGAGCAAGCTGCGCT 933
Db      20  AAGGGGCCCGTCGATGGAAGTGCCCCTTTNAAACCACTCTCTGAAGACCGAGCCGTTT 79

QY      934  CTACCTGC--GGGACGTCATCTCTGGGCTCGAGTACTTGCATCGCCAGAGATCGTCCACA 992
Db      80  CTACTTCCAGGATCTGATCAAAAGGNATCGAGTACTTACACTACCAAGAGATCATCCACC 139

QY      993  GGGACATCAAGCCATCCCAACCTGCTCCCTGGGGGATGATGGGCACTGGAAGATCGCGGACT 1052
Db      140  GTGACATCAAACTTTCAACCTGCTGCTCGGAGAGATGGGACATCAAGATCGGTGACT 199

QY      1053  TTGGCGTCAGCAACCAAGTTTGTAGGGGAGACGAGCTC 1088
Db      200  TTGGTGTGAGCAATGAATTTCAAGGGCAGTGACGCGC 235
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Query Match 4.1%; Score 90.4; DB 4; Length 1302;
Best Local Similarity 50.6%; Pred. No. 4.9e-12;
Matches 335; Conservative 0; Mismatches 306; Indels 21; Gaps 4;

QY 758 GTGTACCAAGGAGTGCCTCTGGAAGAGTGGACCACTGTAATGTCTGTAACCTGATC 817
DB 283 GTGAAGAGGAATTCACACTACTGAGAGGTACGGCACAATAATGTCTCAGCTGGTG 342
QY 818 GAGGTCTCGATGACCCAGCTGAGGACCACTCTATTGTTGTTTGA-----CCTCCTG 871
DB 343 GATGTGTTATACAACGAAGAGAGCAAAATGTATGTGATGAGTACTGCGTGTGT 402
QY 872 AGAAGAGGCGCGTCTATGGAAGTGCCTGTGACAGCCCTTCTCGGAGAGCAAGTCTGC 931
DB 403 GGCATGCGAAGAAATGCTGACACCGCTGCGGAGAGCGTTTCCCATGTGCGCAGGCCAC 462
QY 932 CTCCTACCTGCGGAGCTCATCTGCGSCCTCGAGTACTTGCACCTGCAGAAAGATCTCCAC 991
DB 463 GGTACTTCTGTGCTGATGACGCGCTGGAGTACTCATAGCCAGGCAATTTGTCAC 522
QY 992 AGGACATCAAGCCATCAACCTGTCTCTGGGGGATGATGGCACTGGAAGATCGCCGAC 1051
DB 523 AAGGACATCAAGCGGGGAACCTGTCTCACCACCGGTGGCACCTCAAAATCTCCGAC 582
QY 1052 TTTGCGCTCAGCAACGAGTTTGAGGGGAACGAGCTCAGCTGTCCAGCAGCGC-----G 1105
DB 583 CTGGCGGTGGCGAGGCACTGCACCCGTTTCGGCGGAGCACACCTGCGGACCGCCAG 642
QY 1106 GGAACCCAGCACTTCATGSCCCCGGAGGCACTTCTGATTCGGGCGCAGAGCTTCAGTGG 1165
DB 643 GGCTCCCGGCTTTCAGCGCGCCGAG---ATTGCCAAGCGGCTGGAACCTTCTCCGCG 699
QY 1166 AAGGCTTTGGATGATGGGCACTGCGGTGCACTGTTGTTGTTGTTGTTGTTGTTGTTG 1225
DB 700 TTCAAGGTGGACATCTGGTGGCTGGGGTCACTTCAACATCACCAGCGTCTGTAC 759
QY 1226 CAATTCTGAGGATTTTATCTGCGGCTCCACAGAGATCAAGATGAGCCCGGTGGTG 1285
DB 760 CCTTCGAAGGGGCAACATCTACAAGTTGTTTGAAGATCCGGAGGGGAGCTACGCC 819
QY 1286 TTTCTCTGAGGAGCCAGAAATCAGCGAGGCTCAAGGACCTGATCCTGAAGATGTAGC 1345
DB 820 ATCCCGGGGAGTGTG-----GCCCGCGCTCTCTGACCTGCTGAAGGGGATGCTTGA 873
QY 1346 AAGAAATCCGAGACAGAGAAATGGGGTGGCCAGACATCAAGTTGACCTTTGGGTGACCAAG 1405
DB 874 TACGAACCGGCAAGAGGTTTCTCCATCCGGCAGATCCGGCAGACACAGCTGGTTCCGGAAG 933
QY 1406 AA 1407
DB 934 AA 935

RESULT 9
US-08-749-902-2
; Sequence 2, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0150 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1466 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: Consensus
US-08-749-902-2

Query Match 4.0%; Score 87; DB 2; Length 1466;
Best Local Similarity 50.0%; Pred. No. 3.2e-11;
Matches 331; Conservative 0; Mismatches 310; Indels 21; Gaps 4;

QY 758 GTGTACCAAGGAGTGCCTCTGGAAGAGTGGACCACTGTAATGTCTGTAACCTGATC 817
DB 382 GTGAAGAGGAATTCACACTACTGAGGAGGTACGGCACAATAATGTCTCAGCTGGTG 441
QY 818 GAGGTCTCGATGACCCAGCTGAGCACAACCTCTATTGTTGTTTGA-----CCTCCTG 871
DB 442 GATGTGTTATACAACGAAGAGAGCAAAATGTATGTTGATGAGTACTGCGTGTGT 501
QY 872 AGAAGAGGCGCGCTCATGGAAGTGCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCG 931
DB 502 GGCATGCGAGGAATGCTGGAAGCTGCGGAGAGCGTTTCCAGTGTCCGAGCCAC 561
QY 932 TCTTACTCTCGGAGAGTCACTCTGCGCTCTCGAGTACTTGCACCTGCCAGAAATCGTCCAC 991
DB 562 GGGTACTTCTGTGACCTGATTCAGCGCTGCGGTACTGTCATNGCCAGGNAATTTGTCAC 621
QY 992 AGGACATCAAGCCATCCAACTGCTCTGCGGGGATGATGGCAGTGAAGATCCCGAC 1051
DB 622 AAGGCAATCAAGCGGGGAACCTGCTGCTCACACCGGTGGCACCCCTCAAAATCTCCGAC 681
QY 1052 TTTGCGCTCAGCAACCACTGTTGAGGGGAACGAGCTCAGCTGTCCAGCAGCGC-----G 1105
DB 682 CTGGGCGTGGCGAGGCACTGCACCCGTTGCGGCGGAGCAGACCTGCGGACAGCCAG 741
QY 1106 GGAACCCAGCAATTCATGGCCCCCGAGGCAATTTCTGATTCGCGCAGAGCTTCAGTGG 1165
DB 742 GGTCTCCCGGCTTTCAGCGCGCCGA---NATTGCAACCGGCTCGACACCTTCTCCGCG 798
QY 1166 AAGGCTTTGGATGATGGCCACTGCGCTCAGTTGTACTGTTGTCTATGGGAAGTGC 1225
DB 799 TTCAAGGTGGACATCTGTGCGGTGGGGTCACTCTTCAACATCACCACGCGTCTGTAC 858
QY 1226 CCATTCTCAGAGTTCATCTGCGCCCTCCACAGGAAGATCAAGAAATGAGCCCTGTGTG 1285
DB 859 CCTTCGAAGGGGACAACTCTACAAGTTGTTGAGAACATCGGAAGAGGAGCTACGCC 918
QY 1286 TTTCTCTGAGGAGCCAGAAATCAGCGAGAGTCTCAAGGACCTGATCCTGAAAGTGTAC 1345
DB 919 ATCCCGGGGCACTGTG-----GCCCGCGCTCTCTGACCTGCTGAAAGGATGTTGAG 972
QY 1346 AAGATCCGAGACGAGAAATTTGGGTGGCAGACATCAAGTTGCCACCTTGGGTGACCAAG 1405
DB 973 TACGAACCGGCAAGAGGTTCTCCATCCGGGAGATCCGGCAGCACAGCTGGTTCCGGAAG 1032
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QY 1406 AA 1407
Db 1033 AA 1034

RESULT 10
US-08-685-852-1
; Sequence 1, Application US/08685852
; Patent No. 6660837
; GENERAL INFORMATION:
; APPLICANT: KAIBUCHI, KOZO
; APPLICANT: ONO, YOSHITAKA
; APPLICANT: IWAMATSU, AKIHIRO
; TITLE OF INVENTION: MODIFIED PROTEIN DERIVED FROM PROTEIN KINASE N
; FILE REFERENCE: 016887/0844
; CURRENT APPLICATION NUMBER: US/08/685,852
; CURRENT FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: JP 7-262552
; PRIOR FILING DATE: 1995-09-14
; PRIOR APPLICATION NUMBER: JP 7-344606
; PRIOR FILING DATE: 1995-12-05
; PRIOR APPLICATION NUMBER: JP 8-080549
; PRIOR FILING DATE: 1996-03-08
; PRIOR APPLICATION NUMBER: JP 8-114226
; PRIOR FILING DATE: 1996-04-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)..(2862)
US-08-685-852-1

Query Match 3.8%; Score 83.8; DB 4; Length 2968;
Best Local Similarity 54.8%; Pred. No. 2.3e-10;
Matches 166; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 841 GGACAACTCTATTGGTGTGTTGACCTCTGAGAAAGGGGCGGCTCATGGAAGTGCCTG 900
Db 2100 GGAGCAGCTGTGCTCGTGTGAGTACTCGCGCGGTGGGACCTGATGCTGCACATCCA 2159

QY 901 TGACAAGCCCTTTCGGAGAGAGAGCTCGCTCTACCTGCGGAGACGTCATCTGGGCGCT 960
Db 2160 CAGCGACGTGTCTCTGAGCCCGTGCCATCTTTTATTCGCGCTGCGTGTGCTGGGCGCT 2219

QY 961 CGAGTACTTGCACTGCCAGAGATCGTCCACAGGGACATCAAGCCATCCCAACCTGCTCCT 1020
Db 2220 ACAGTTTCTTACGAAACACAGATCGTCTACAGGAGCTGAGTTGGACAAATTGCTCCT 2279

QY 1021 GGGGGATGATGGGACGCTGAAGATCGCCGACTTTGGCGTCAGCAACCAAGTTTGAGGGAA 1080
Db 2280 GGACACCGAGGGCTACGTCAGATCGCAGACTTTGGGCTCTGCAAGGAGGGGATGGGCTA 2339

QY 1081 CGAGCTCAGCTGTCAGACGCGGGGAAACCCAGCATTCATGGCCCCCGAGGCCATTTC 1140
Db 2340 TGGGACCGGACCAAGCACAATCTGTGGGACCCCGAGTTCTTGGCCCCCTGAGGTGCTGAC 2399

QY 1141 TGA 1143
Db 2400 GGA 2402

RESULT 11
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
```

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; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1

Query Match 3.8%; Score 83.4; DB 3; Length 1599;
Best Local Similarity 51.3%; Pred. No. 2.3e-10;
Matches 254; Conservative 0; Mismatches 226; Indels 15; Gaps 2;

QY 878 GGGCCCCGTCATGGAAGTGCCCTGTGCAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTAC 937
Db 793 GAGCTGTTCTTCCACCTGTCCCGGAGCGTGTCTTACAGAGGAGCGGCGCCGTTTAT 852

QY 938 CTGCGGACGTCATCTCGGCGCTCGAGTACTTGCATGCGCAGAGATCGTCCACAGGAC 997
Db 853 GGTGCAGAGATTGTCTCGGCTCTTGAAGTACTTGCATCTCGGCGGACGTGTATACCGGAC 912

QY 998 ATCAAGCCATCCCAACCTGCTCTGGGGATGATGGGACGTGAAGATCGCGACTTTGGC 1057
Db 913 ATCAAGCTGGAACCTCATGCTGGACAAAGATGGCCACATCAAGATCACTGACTTTGGC 972

QY 1058 GTCAGCAACCAAGTTTGAGGGGAAACGCGCTCAGCTGTCTCCAGCAGCGGGAACCCAGCA 1117
Db 973 CTCTGCAAGAGGGCATCAGTGACGGGGCCACCATGAACCTTCTGTGGGACCCCGAG 1032

QY 1118 TTCAATGCCCCCGAGGCGCATTTCTGATTCGCGCAGAGCTTCAGTGGGAAGGCCCTTGAT 1177
Db 1033 TACCTGGCGCTGAGGTGCTGGAGGACATGACTA-----TGGCCGCGCGTGGAC 1083

QY 1178 GTATGGCCACTGCGCTCAGCTTGTGCTGTCTATGGAAGTCCCATTCATCGAC 1237
Db 1084 TGTGGGGGTGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143

QY 1238 GATTTCATCTGCGCCTCCACAGGAAGATCAAGAATGAGCCCGTGTGTTCCTGAGGAG 1297
Db 1144 CAGGACCAAGCGCGCTCTTCGAGCTCATCTCATGGAAGATCCCGCTTCCC-----G 1197

QY 1298 CAGAAATACGAGGAGCTCAAGGACCTGATCTCTGAAGATGTTAGACAAGATCCCGAG 1357
Db 1198 CGCAGCTCAGCCCCGAGGCAAGTCCCTGCTTGTGGGCTGCTTAAAGAGGACCCCAAG 1257

QY 1358 ACGAGAACTGGGTG 1372
Db 1258 CAGAGGCTTGTGGG 1272

RESULT 12
US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 636151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorghna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-167-322-3

Query Match 3.8%; Score 83.4; DB 4; Length 1599;
Best Local Similarity 51.3%; Pred. No. 2.3e-10;
Matches 254; Conservative 0; Mismatches 226; Indels 15; Gaps 2;

QY 878 GGGCCCGTCATGGAAGTGCCTGTGCAAGCCCTTCTCGAGAGCAAGCTCGCCTCTAC 937
Db 793 GAGCTGTTCTTCCACCTGTCCCGGAGCGTGTCTTCACAGAGGAGCGGCGCGTTTAT 852

QY 938 CTGCGGGAGCTCATCTCGGCGCTCGAGTACTTGCAAGATCGTCACAAGGAC 997
Db 853 GGTGACAGATTGTCTCGGCTCTTGAGTACTTGCACTCGGGAGCGTGTATACCGAC 912

QY 998 ATCAAGCCATCAACCTGCTCTCGGGGATGATGGGACGTGAAGATCGCGACTTTGC 1057
Db 913 ATCAAGCTGGAAGAACCTCATGCTGGACAAAGATGCCACATCAAGATCACTGACTTGC 972

QY 1058 GTCAAGAACCAATTTGAGGGAAACAGCGTCAAGTGTTCAGACGCGGGAAACCCAGCA 1117
Db 973 CTCTGAAAGAGGATCAGTACGCGGGCCACCATGAAACCTTCTGTGGACCCCGGAG 1032

QY 1118 TTCAATGGCCCGAGGCCATTTCTGATTCGCGCCAGAGCTTCAGTGGGAAGCGCTTGGAT 1177
Db 1033 TACCTGGCGCCTGAGGTGCTGGAGGACATGACTA-----TGGCGGCGCGTGGAC 1083

QY 1178 GTATGGGCGCCTGGCGCTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCTTTCATCGAC 1237
Db 1084 TGGTGGGCGCTGGTGTGTCTATGACGAGATGATGCGGCGCGCTGCGCTTCTACAC 1143

QY 1238 GATTTTCATCTGCGCTTCCACAGGAAGATCAAGATGAGCCCGTGTGTTTCTTAGAGG 1297
Db 1144 CAGGACACGAGCGCTTCTTCGAGTCTATCTCATGCTCATGCTGAGGAGATCGCTTCCG 1197

QY 1298 CCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCCTGAAGATGTTAGCAAGATCCCGAG 1357
Db 1198 CGACGCTCAGCCCCGAGGCCAAGTCCCTGCTGTTGGGTGCTGTTAAGAGGACCCCAAG 1257

QY 1358 ACAGAAATGGGGTG 1372
Db 1258 CAGAGGCTTGGTGGG 1272

RESULT 13
US-09-023-655-1004
; Sequence 1004, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
;
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1004:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178325
; US-09-023-655-1004

Query Match 3.8%; Score 83.4; DB 4; Length 1599;
Best Local Similarity 51.3%; Pred. No. 2.3e-10;
Matches 254; Conservative 0; Mismatches 226; Indels 15; Gaps 2;

QY 878 GGGCCCGTCATGGAAGTGCCTGTGCAAGCCCTTCTCGAGAGCAAGCTCGCCTCTAC 937
Db 793 GAGCTGTTCTTCCACCTGTCCCGGAGCGTGTCTTCACAGAGGAGCGGCGCGTTTAT 852

QY 938 CTGCGGGAGCTCATCTCGGCGCTCGAGTACTTGCAAGATCGTCACAAGGAC 997
Db 853 GGTGACAGATTGTCTCGGCTCTTGAGTACTTGCACTCGGGAGCGTGTATACCGAC 912

QY 998 ATCAAGCCATCAACCTGCTCTCGGGGATGATGGGACGTGAAGATCGCGACTTTGC 1057
Db 913 ATCAAGCTGGAAGAACCTCATGCTGGACAAAGATGCCACATCAAGATCACTGACTTGC 972

QY 1058 GTCAAGAACCAATTTGAGGGAAACAGCGTCAAGTGTTCAGACGCGGGAAACCCAGCA 1117
Db 973 CTCTGAAAGAGGATCAGTACGCGGGCCACCATGAAACCTTCTGTGGACCCCGGAG 1032

QY 1118 TTCAATGGCCCGAGGCCATTTCTGATTCGCGCCAGAGCTTCAGTGGGAAGCGCTTGGAT 1177
Db 1033 TACCTGGCGCCTGAGGTGCTGGAGGACATGACTA-----TGGCGGCGCGTGGAC 1083

QY 1178 GTATGGGCGCCTGGCGCTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCTTTCATCGAC 1237
Db 1084 TGGTGGGCGCTGGTGTGTCTATGACGAGATGATGCGGCGCGCTGCGCTTCTACAC 1143

QY 1238 GATTTTCATCTGCGCTTCCACAGGAAGATCAAGATGAGCCCGTGTGTTTCTTAGAGG 1297
Db 1144 CAGGACACGAGCGCTTCTTCGAGTCTATCTCATGCTCATGCTGAGGAGATCGCTTCCG 1197

QY 1298 CCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCCTGAAGATGTTAGCAAGATCCCGAG 1357
Db 1198 CGACGCTCAGCCCCGAGGCCAAGTCCCTGCTGTTGGGTGCTGTTAAGAGGACCCCAAG 1257

QY 1358 ACAGAAATGGGGTG 1372
Db 1258 CAGAGGCTTGGTGGG 1272

RESULT 13
US-09-023-655-1004
; Sequence 1004, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
;
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1004:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178325
; US-09-023-655-1004
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Db 1144 CAGGACACAGAGCCCTCTTCGAGCTCATCTCTAATGAAGAGATCCGCTTCCC-----G 1197
Qy 1298 CCAGAAATCAGCGAGGAGCTCAAGGACCTGATCTCTGAAGATGTTAGACAAGATCCCGAG 1357
Db 1198 CGCAGCTCAGCCCGAGGCCAAGTCCCTGCTTCTGCTGGCTGCTTAAGAAGGACCCCAAG 1257
Qy 1358 ACAGAAATGGGGTG 1372
Db 1258 CAGAGGCTTGTTGGG 1272

RESULT 14

US-09-799-875-15
; Sequence 15, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT FILING DATE: 2001-03-06
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-875-15

Query Match 3.8%; Score 82.8; DB 4; Length 1257;
Best Local Similarity 53.1%; Pred. No. 3e-10;
Matches 224; Conservative 0; Mismatches 192; Indels 6; Gaps 2;
Qy 758 GTGTACAGAGATGTCCTCTGAAGAAGCTGGACCACTGGAATGTTGGTCAAACTGATC 817
Db 211 GTCTTCGGGAGCTGGAGATCTCTCAGGAGATCGAGCAGCTTCTCTCTGGTGAACCTCTGG 270
Qy 818 GAGTCTCTGATGATCCAGCTGAGGACAACTCTATTTGTTGTTGACCTCTCTGAGAAG 877
Db 271 TACTCTCTCAGGAGAC---GAGGAGGACATGTTATGTTCTGGACCTGCTACTGGGCGGG 327
Qy 878 GGGCCCTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCTCTAC 937
Db 328 GACCTGGCTTACCACCTCGACAGAAAGTGCAGTTCTCCGAGGACACGGTGAAGCTGTAC 387
Qy 938 CTGCGGAGCTCATCTCTGGGCTCGAGTATTGCACTGCCAGAAAGATGTTCCACAGGGAC 997
Db 388 ATCTCGAGATGGCACTGGCTCTGGACTACTCTGGCGGCCAGCACATCATCCACAGAGAT 447
Qy 998 ATCAAGCCATCCAACTCTCTGGGGATGATGGGACGTGAGATCGCGGACTTTGGC 1057
Db 448 GTCAAGCTTCACAACTTCTCTGGATGAGAGGACATGCACACCTGACCGACTTCAAC 507
Qy 1058 GTCAGCAACCAAGTTTGAAGGGAAGCAGCTCAGCTGTCCAGCAGCGGGGAACCCAGCA 1117
Db 508 ATTGCCACCATCATCAAGG---ACGGGAGCGGGCAGCGCATTTAGCAGGACCAAGCCG 564
Qy 1118 TTATGCCCCCGAGGCCATTTCTGATTCGGCCAGAGCTTCAGTGGGAAGCCCTTGGAT 1177
Db 565 TACATGGCTCCGAGATCTTCCACTCTTTGTTCAACGGCGGACCCGCTACTCTCTCGAG 624
Qy 1178 GT 1179
Db 625 GT 626

RESULT 15

US-09-799-875-13
; Sequence 13, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT FILING DATE: 2001-03-06
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)...(1273)
US-09-799-875-13

Query Match 3.8%; Score 82.8; DB 4; Length 1826;
Best Local Similarity 53.1%; Pred. No. 3.4e-10;
Matches 224; Conservative 0; Mismatches 192; Indels 6; Gaps 2;
Qy 758 GTGTACAGAGATGTCCTCTGAAGAAGCTGGACCACTGGAATGTTGGTCAAACTGATC 817
Db 227 GTCTTCGGGAGCTGGAGATCTCTCAGGAGATCGAGCAGCTTCTCTCTGGTGAACCTCTGG 286
Qy 818 GAGTCTCTGATGATCCAGCTGAGGACAACTCTATTTGTTGTTGACCTCTCTGAGAAG 877
Db 287 TACTCTCTCAGGAC---GAGGAGGACATGTTATGTTCTGGACCTGCTACTCTGGCGGG 343
Qy 878 GGGCCCTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCTCTAC 937
Db 344 GACCTGGCTTACCACCTGCAGCAGAAAGTGCAGTTCTCCGAGGACACGGTGAAGCTGTAC 403
Qy 938 CTGCGGAGCTCATCTCTGGGCTCGAGTATTGCACTGCCAGAAAGATGTTCCACAGGGAC 997
Db 404 ATCTCGAGATGGCACTGGCTCTGGACTACTCTGGCGGCCAGCACATCATCCACAGAT 463
Qy 998 ATCAAGCCATCCAACTCTCTGGGGATGATGGGCACTGGAAGATCGCGACTTTTGGC 1057
Db 464 GTCAAGCTTCACAACTTCTCTGGATGAGAGGACATGCACACTGACCGACTTCAAC 523
Qy 1058 GTCAGCAACCAAGTTTGAAGGGAACGACGCTCAGCTGTCCAGCAGCGGGGAACCCAGCA 1117
Db 524 ATTGCCACCATCATCAAGG---ACGGGAGCGGGCAGCGCATTTAGCAGGACCAAGCCG 580
Qy 1118 TTATGCCCCCGAGGCCATTTCTGATTCGGCCAGAGCTTCAGTGGGAAGCCCTTGGAT 1177
Db 581 TACATGGCTCCGAGATCTTCCACTCTTTGTTCAACGGCGGACCCGCTACTCTCTCGAG 640
Qy 1178 GT 1179
Db 641 GT 642

Search completed: July 12, 2004, 01:20:51
Job time : 186 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 17:43:52 ; Search time 1238 Seconds
(without alignments)
7514.987 Million cell updates/sec

Title: US-10-690-617-1

Perfect score: 2190

Sequence: 1 cgcgcgggctgagctcgg.....ctcttgctattcagacgct 2190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002s: *
7: Geneseqn2003as: *
8: Geneseqn2003bs: *
9: Geneseqn2003cs: *
10: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	2001.6	91.4	3501	5	AAD08635 Human kin
3	1906.4	87.1	1937	6	AAD30566 Human kin
4	1636.2	74.7	2711	6	ABK49563 Human cDN
5	1610.2	73.5	2018	6	ABZ11551 Human pol
6	1601.4	73.1	1611	6	ABX97035 Human NOV
7	1493.8	68.2	1547	6	ABX97034 Human NOV
8	1475.8	67.4	1725	6	ABX97036 Human NOV
9	1461.8	66.7	1542	4	AA306710 Polynucle
10	1366.8	62.4	3411	9	ADB53308 Primary r
11	661	30.2	2545	3	AAZ29223 Human cel
12	651.2	29.7	4942	9	ADB75227 Prostate
13	651	29.7	1804	6	ABX92170 Prostate
14	651	29.7	1804	9	ADB75229 Prostate
15	645.6	29.5	2056	4	AAI57819 Human pol
16	644	29.4	1767	4	AAE44686 Novel pro
17	641.6	29.3	4982	7	ABX34704 Human mod
18	585.6	26.7	2268	4	AAI59606 Human pol
19	585.6	26.7	2268	4	AAI59605 Human pol
20	572	26.1	731	4	AAH99185 Human pro
21	561.4	25.6	29629	6	ABL58699 Human kin
22	529.6	24.2	705	4	AA527190 cDNA enco
23	529.6	24.2	705	4	ABK43592 DNA encod

24	529.6	24.2	705	9	ADB93368
25	526	24.0	2411	9	ADC99145
26	518	23.7	1927	4	AAI57820
27	395.8	18.1	432	9	ADB85632
28	389.4	17.8	1854	3	AA78427 Human sec
29	348.8	15.9	439	4	AAH99412 Human pro
30	283	12.9	331	3	AAC02673 Human sec
31	274.6	12.5	876	6	ABK34394 Human cDN
32	262.6	12.0	491	8	ACH14059 Human adu
33	244.6	11.2	485	8	ACH15568 Human adu
34	202.4	9.2	1174	4	ABL19199 Drosophil
35	201.2	9.2	469	4	AAI15690 Probe #56
36	201.2	9.2	469	4	ABA57768 Human foe
37	201.2	9.2	469	4	AAI37350 Probe #60
38	201.2	9.2	469	4	ABA27140 Probe #56
39	201.2	9.2	469	4	AAK31464 Human bon
40	201.2	9.2	469	4	AAK05833 Human bra
41	201.2	9.2	469	4	ABS31146 Human liv
42	201.2	9.2	469	6	ABS06218 Human gen
43	201.2	9.2	10800	4	AAK83329 Human imm
44	201	9.2	218	4	AAI24914 Probe #14
45	201	9.2	218	4	ABA70385 Human foe

ALIGNMENTS

RESULT 1

ABL58698

ID ABL58698 standard; cDNA; 2190 BP.

XX

AC ABL58698;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human kinase encoding cDNA.

XX

KW Human; kinase protein; calcium/calmodulin-dependant protein kinase; eye;
retinoblastoma; brain; kinase modulator; gene; SNP;
single nucleotide polymorphism; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT 5'UTR

FT CDS

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PT a disease or predisposition to the disease mediated by the peptide.

XX Claim 4b; Fig 1; 89pp; English.

XX The invention relates to an isolated peptide designated human kinase (HK), that has homology to members of the calcium/calmodulin-dependent protein kinase kinase subfamily. The mechanism of action of the protein of the invention is that of a kinase modulator. The human kinase of the invention is useful for creating a pharmaceutical composition for treating a disease or condition mediated by the human kinase. HK is also useful to provide a target for diagnosing a disease or predisposition to disease mediated by HK, and is also useful in pharmacogenetic analysis. HK is useful for treating a disorder characterised by absence of inappropriate or unwanted expression of HK, also as an immunogen to raise antibodies by administering HK to a mammalian organism e.g. rat, rabbit or mouse. Nucleic acids of the invention are useful as hybridisation probes for mRNA, transcript/cDNA and genomic DNA. Recombinant host cells expressing a native HK are useful for assaying compounds that stimulate or inhibit HK function. Nucleic acids of the invention are also useful for producing transgenic animals. Experimental data indicates that kinase proteins of the present invention are expressed in humans in the eye (retinoblastomas) and brain. The current sequence represents cDNA encoding the human kinase of the invention

SQ Sequence 2190 BP; 457 A; 655 C; 708 G; 370 T; 0 U; 0 Other;

Query Match 100.0%; Score 2190; DB 6; Length 2190;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGCCGCGGGGTGAGCTCGGCGATCTGGGCCCCAGCGAGGCGGTGGGGCGGGGCGGCGG	60
DB	1	CGCCCGCGGGGTGAGCTCGGCGATCTGGGCCCCAGCGAGGCGGTGGGGCGGGGCGGCGG	60
QY	61	GGGGGGGGCGGCGAGCGAGGAGTGGGGGGCGCGCGCGGGGCCACGACACTGTGCGCC	120
DB	61	GGGGGGGGCGGCGAGCGAGGAGTGGGGGGCGCGCGCGGGGCCACGACACTGTGCGCC	120
QY	121	GGGGCGGAGTTCACAGAGCTACGACAGAGAACCCCTTGACTGAAGCAATGGAGGG	180
DB	121	GGGGCGGAGTTCACAGAGCTACGACAGAGAACCCCTTGACTGAAGCAATGGAGGG	180
QY	181	GGGTCCAGCTGTCTGCTCCAGGATCTCGGCGAGAGCTGTAGAACGGGTGGCAGCCAT	240
DB	181	GGGTCCAGCTGTCTGCTCCAGGATCTCGGCGAGAGCTGTAGAACGGGTGGCAGCCAT	240
QY	241	CGATGTGACTCACTTGGAGGAGGAGATGGTGGCCAGAGCCTACTAGAAACGGTGTGGA	300
DB	241	CGATGTGACTCACTTGGAGGAGGAGATGGTGGCCAGAGCCTACTAGAAACGGTGTGGA	300
QY	301	CCCCCAGCAGGGGCGAGCTGCTCTGTGATCCCTGGCAGTACTCAAGACTGCTCCC	360
DB	301	CCCCCAGCAGGGGCGAGCTGCTCTGTGATCCCTGGCAGTACTCAAGACTGCTCCC	360
QY	361	AGCCGGCTAGCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGCAGGAAGCTA	420
DB	361	AGCCGGCTAGCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGCAGGAAGCTA	420
QY	421	TCTGAGGCGCAGGCTGGGCTTTATGCAACGGGGCTGCCAGCCACATCTCCCCCGGGC	480
DB	421	TCTGAGGCGCAGGCTGGGCTTTATGCAACGGGGCTGCCAGCCACATCTCCCCCGGGC	480
QY	481	CTGGGGAGGCCCCCATCGAGTCCACACGTGGCCATCTCAGATGACAGGAGCTGCGT	540
DB	481	CTGGGGAGGCCCCCATCGAGTCCACACGTGGCCATCTCAGATGACAGGAGCTGCGT	540
QY	541	GCAGTGAACCAAGTACAAAGCTGCGAGTGAGATTGGCAAGGCTGCTACGGTGTGGTGAG	600
DB	541	GCAGTGAACCAAGTACAAAGCTGCGAGTGAGATTGGCAAGGCTGCTACGGTGTGGTGAG	600
QY	601	GCTGGCCTACAAAGAGTGAAGACAGACACTATGCAATGAAGTCTTCCAAAAGAA	660
DB	601	GCTGGCCTACAAAGAGTGAAGACAGACACTATGCAATGAAGTCTTCCAAAAGAA	660

QY	661	GTTACTGAGCAGTATGGCTTTCCAGTGGCCCTCCCGCAGAGGGTCCCGAGGTGCGCA	720
DB	661	GTTACTGAGCAGTATGGCTTTCCAGTGGCCCTCCCGCAGAGGGTCCCGAGGTGCGCA	720
QY	721	GGGAGGACACAGCAAGCAGCTGCTGCCCTGGAGCGGTGTACACAGAGATGTGCATCCT	780
DB	721	GGGAGGACACAGCAAGCAGCTGCTGCCCTGGAGCGGTGTACACAGAGATGTGCATCCT	780
QY	781	GAAGAAGCTGGAACACCACTGAATGTGGTCAAACTGATCGAGGTCTTGAGATGACCCAGCTGA	840
DB	781	GAAGAAGCTGGAACACCACTGAATGTGGTCAAACTGATCGAGGTCTTGAGATGACCCAGCTGA	840
QY	841	GGACAACTCTATTGTGTGTGGTCACTTGGACCTTGGAGAAAGGGGCCCTCATGGAAGTGGCCCTG	900
DB	841	GGACAACTCTATTGTGTGTGGTCACTTGGACCTTGGAGAAAGGGGCCCTCATGGAAGTGGCCCTG	900
QY	901	TGACAAAGCCCTTCTCGGAGGAGCAAGCTCGCCTTACCTGCGGACGTCATCTCTGGGCT	960
DB	901	TGACAAAGCCCTTCTCGGAGGAGCAAGCTCGCCTTACCTGCGGACGTCATCTCTGGGCT	960
QY	961	CGAGTACTTGCACTGCGCAGAAGATCGTCCAAGGAGCATCAAGGCATCAACCTGCTCT	1020
DB	961	CGAGTACTTGCACTGCGCAGAAGATCGTCCAAGGAGCATCAAGGCATCAACCTGCTCT	1020
QY	1021	GGGGGATGATGGGCACTGAGATCGCGGCTTTGGGTGTCAGCAACCAAGTTTGAGGGGAA	1080
DB	1021	GGGGGATGATGGGCACTGAGATCGCGGCTTTGGGTGTCAGCAACCAAGTTTGAGGGGAA	1080
QY	1081	CGACGCTCAGCTGTCCAGCAGCGCGGAAACCCAGCATTATGCGCCCCCGAGGCCATTTC	1140
DB	1081	CGACGCTCAGCTGTCCAGCAGCGCGGAAACCCAGCATTATGCGCCCCCGAGGCCATTTC	1140
QY	1141	TGATTCGCGCCAGACTTTCAGTGGGAAGCCCTTGATGTATGGGCACTGCGGTCACGTT	1200
DB	1141	TGATTCGCGCCAGACTTTCAGTGGGAAGCCCTTGATGTATGGGCACTGCGGTCACGTT	1200
QY	1201	GTACTGTTGTTCTATGGGAAGTCCCATTCATCGACGATTTCTCTGGCCCTCCACAG	1260
DB	1201	GTACTGTTGTTCTATGGGAAGTCCCATTCATCGACGATTTCTCTGGCCCTCCACAG	1260
QY	1261	GAAGATCAAGAATGAGCCCGTGTGTTTCTGAGAGCGCAAAATCAGCGAGGAGCTCAA	1320
DB	1261	GAAGATCAAGAATGAGCCCGTGTGTTTCTGAGAGCGCAAAATCAGCGAGGAGCTCAA	1320
QY	1321	GGACCTGATCTGGAAGATTTAGACAGAAATCCCGAGACGAAATTTGGGTGCCAGACAT	1380
DB	1321	GGACCTGATCTGGAAGATTTAGACAGAAATCCCGAGACGAAATTTGGGTGCCAGACAT	1380
QY	1381	CAAGTTGCACCTTTGGGTGACCAAGAACGGGGAGGAGCCCTTCTTCGAGGAGGAGCA	1440
DB	1381	CAAGTTGCACCTTTGGGTGACCAAGAACGGGGAGGAGCCCTTCTTCGAGGAGGAGCA	1440
QY	1441	CTGACGCTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAG	1500
DB	1441	CTGACGCTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAG	1500
QY	1501	CTGACACACGCTGTGCTGTGAGTCCATCTGAGGAGGCTTCTTTGGGAACCCGTT	1560
DB	1501	CTGACACACGCTGTGCTGTGAGTCCATCTGAGGAGGCTTCTTTGGGAACCCGTT	1560
QY	1561	TGAGCCCCCAGCAGCGGAGGAGGAGCGATCCATGTCTGCTCCAGGAAACCTTACTGGTGA	1620
DB	1561	TGAGCCCCCAGCAGCGGAGGAGGAGCGATCCATGTCTGCTCCAGGAAACCTTACTGGTGA	1620
QY	1621	AGAGGGTGTGGTGAAGGGGCAAGAGCCAGAGCTCCCCGGGCTCCAGGAGACGAGGC	1680
DB	1621	AGAGGGTGTGGTGAAGGGGCAAGAGCCAGAGCTCCCCGGGCTCCAGGAGACGAGGC	1680
QY	1681	TGCATCTGAGCCCTGCATGACCCAGGGGACCCCGGACACACTCATCTCCGGGCTC	1740
DB	1681	TGCATCTGAGCCCTGCATGACCCAGGGGACCCCGGACACACTCATCTCCGGGCTC	1740

QY 1741 CAGAGGCCACCCCTCATGCAACAGCGCCCCCGCAGGACGGGGCTGGGACTGCAGCC 1800
Db |||||
QY 1741 CAGAGGCCACCCCTCATGCAACAGCGCCCCCGCAGGACGGGGCTGGGACTGCAGCC 1800
Db |||||
QY 1801 CCACTCCCGCCCTCCCTCCATCGTGTGATGACCTCCAGCAGCAGCGTCCAGGACAG 1860
Db |||||
QY 1801 CCACTCCCGCCCTCCCTCCATCGTGTGATGACCTCCAGCAGCAGCGTCCAGGACAG 1860
Db |||||
QY 1861 ACTGGAATGTATGTCATTTGGGGCTTTGGGGCAGGGCTCCACAGGAGCCATCCTCTCT 1920
Db |||||
QY 1921 TCTTGSCCTCTTGCCCTGACCCATTCTGTGGGAAACCGGCTGCCATGAGCCTCAG 1980
Db |||||
QY 1921 TCTTGSCCTCTTGCCCTGACCCATTCTGTGGGAAACCGGCTGCCATGAGCCTCAG 1980
Db |||||
QY 1981 AAATGCCACCCCGCTGGTGGCATGCGCTGGGGCAGGACGAGCAGGACCAAGAT 2040
Db |||||
QY 1981 AAATGCCACCCCGCTGGTGGCATGCGCTGGGGCAGGACGAGCAGGACCAAGAT 2040
Db |||||
QY 2041 GGCAGGTGAGGCGCAGGCTTACCAACGGAAGAGACCTCCCGCTGGGGCCGGGACGGCC 2100
Db |||||
QY 2041 GGCAGGTGAGGCGCAGGCTTACCAACGGAAGAGACCTCCCGCTGGGGCCGGGACGGCC 2100
Db |||||
QY 2101 TGGCTCAGCTGCCACAGGATATGTTGGAGGGGGGTACCTGCCACCTTGGGGTGT 2160
Db |||||
QY 2101 TGGCTCAGCTGCCACAGGATATGTTGGAGGGGGGTACCTGCCACCTTGGGGTGT 2160
Db |||||
QY 2161 GGCACACAGAGCTCTTGTCTATTACAGCGCT 2190
Db |||||
QY 2161 GGCACACAGAGCTCTTGTCTATTACAGCGCT 2190
Db |||||

RESULT 2

AA08635
ID AAD08635 standard; cDNA; 3501 BP.
AC AAD08635;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human kinase (PKIN)-2 cDNA.
XX
KW Human kinase; PKIN-2; therapy; immune disorder; Addison's disease; AIDS;
KW acquired immune deficiency syndrome; growth and developmental disorder;
KW arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;
KW leukaemia; cardiovascular disease; myocardial infarction; hypertension;
KW lipid disorder; cancer; fatty liver; cholestasis; transgenic animal;
KW gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological;
KW antidiabetic; nephroprotective; antiulcer; antiarthritic; antirheumatic;
KW antipsoriatic; neuroprotective; cytosstatic; hepatotropic; osteopathic;
KW vasotropic; antianginal; anorectic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 65..1606
FT /*tag= a
FT /product= "Human kinase (PKIN)-2"
XX
PN WO200146397-A2.
XX
PD 28-JUN-2001.
XX
PF 20-DEC-2000; 2000WO-US035304.
XX
PR 23-DEC-1999; 99US-0172066P.
PR 14-JAN-2000; 2000US-0176107P.
PR 21-JAN-2000; 2000US-0177731P.
PR 28-JAN-2000; 2000US-0178573P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX

PI Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R;
PI Yue H, Yao MG, Lal P, Khan FA;
XX WPI; 2001-418059/44.
XX P-PSDB; AAE04361.
XX
XX Novel human kinase proteins (PKIN) useful for diagnosing, treating,
XX preventing immune disorders, cardiovascular diseases and disorders
XX affecting growth and development associated with abnormal expression of
XX PKIN.
XX
XX Claim 5; Page 119-120; 128pp; English.
XX
XX The invention relates to novel human kinase proteins (PKIN) and nucleic
XX acid molecules encoding them. PKIN is useful for identifying compounds
XX that modulates its activity. PKIN cDNA is useful for assessing toxicity
XX of a test compound. PKIN and its cDNA are useful for diagnosis,
XX prevention and treatment of immune disorders such as acquired immune
XX deficiency syndrome (AIDS), Addison's disease, anaemia, adult respiratory
XX distress syndrome, allergies, amyloidosis, psoriasis, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, multiple sclerosis, asthma,
XX osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis
XX and diabetes mellitus; growth and developmental disorders such as atnic
XX keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis,
XX hepatitis, mixed connective tissue disease (MCTD), and myelofibrosis;
XX cancers such as adenocarcinoma and leukaemia, cardiovascular diseases
XX such as myocardial infarction and hypertension; and lipid disorders such
XX as fatty liver and cholestasis. PKIN cDNA is useful to detect upstream
XX sequences such as promoters and regulatory elements, for creating knock
XX in or knock out in humanised animals or transgenic animals to model human
XX disease and for somatic or germline gene therapy for treating the above
XX mentioned disorders. The present sequence is human kinase (PKIN)-2
XX encoding cDNA
XX

SQ Sequence 3501 BP; 763 A; 974 C; 1058 G; 706 T; 0 U; 0 Other;

Query Match 91.4%; Score 2001.6; DB 5; Length 3501;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 4; Indels 30; Gaps 2;
QY 130 GTTCCCAACAGGCTACGAGAACCCCTTGAAGCAATGAGAGGGGGTCCAGC 189
Db |||||
QY 190 TGTCTGCTGCCAGGATCTCGGGCAGAGCTGTAGAACGGGTGGCAGCCATCGATGTGAC 249
Db |||||
QY 82 TGTCTGCTGCCAGGATCTCGGGCAGAGCTGTAGAACGGGTGGCAGCCATCGATGTGAC 141
QY 250 TCACCTTGAGGAGGAGATGTGGCCAGAGCCTACTAGAAACGGTGTGGACCCCCACC 309
Db |||||
QY 142 TCACCTTGAGGAGGAGATGTGGCCAGAGCCTACTAGAAACGGTGTGGACCCCCACC 201
QY 310 ACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCGGCC 369
Db |||||
QY 202 ACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCGGCC 261
QY 370 TAGCCTCTCAGCCAGGAGCTTTCCTACAGAGCGGGCCAGCAGGAAGCTATCTGAGGC 429
Db |||||
QY 262 TAGCCTCTCAGCCAGGAGCTTTCCTACAGAGCGGGCCAGCAGGAAGCTATCTGAGGC 321
QY 430 GCAGGCTGGGCTTATGCGACGGGGCTGCCAGCCACATCTCCCCCGGGCTTGGCGGAG 489
Db |||||
QY 322 GCAGGCTGGGCTTATGCGACGGGGCTGCCAGCCACATCTCCCCCGGGCTTGGCGGAG 381
QY 490 GCCCACCATCGAGTCCCAACCGCTGCGCATCTTCAGATCGAGGAGCTGGTCCAGCTGAA 549
Db |||||
QY 382 GCCCACCATCGAGTCCCAACCGCTGCGCATCTTCAGATCGAGGAGCTGGTCCAGCTGAA 441
QY 550 CCAGTACAGCTGCGAGAGTGAGATTGGCA-----AGG 582
Db |||||
QY 442 CCAGTACAGCTGCGAGAGTGAGATTGGCAAGGTGGGCTGACTGATGCTTCTCGAGGG 501
QY 583 TGCCTACGGTGTGGAGGCTGGCCCTCAACGAAAGTGAAGACAGACACTATGCAATGAA 642

|||||
502 TGCCTACGGTGTGGTGGCTTCAACAAAGTGAAGACAGACATATGACATGAA 561
|||||
643 AGTCCTTTTCAAAAAGAGTTACTGAAGCAGTATGGCTTTCCACGTGCGCCCTCCCCCGAG 702
|||||
562 AGTCCTTTTCAAAAAGAGTTACTGAAGCAGTATGGCTTTCCACGTGCGCCCTCCCCCGAG 621
|||||
703 AGGTCCTCAGGCTGCCAGGGAGACACAGCCAGCAGCTGTGCGCCCTGGAGCGGGTGA 762
|||||
622 AGGTCCTCAGGCTGCCAGGGAGACACAGCCAGCAGCTGTGCGCCCTGGAGCGGGTGA 681
|||||
763 CCAGCAGATTCCCATCTCTGAAGAAGCTGGACACGTGAATGTGTCAAACTGATCGAGGT 822
|||||
682 CCAGCAGATTGCCATCTCTGAAGAAGCTGGACACGTGAATGTGTCAAACTGATCGAGGT 741
|||||
823 CCTGGATGACCCAGCTGAGGCAACCTCTATTGCTGTTTGAACCTCTCTGAGAAAGGGGCC 882
|||||
742 CCTGGATGACCCAGCTGAGGCAACCTCTATTGCTGTTTGAACCTCTCTGAGAAAGGGGCC 798
|||||
883 GGTATGGAAGTGCCTGTGACAGCCCTTCTCGAGGAGCAAGCTGCGCTTACCTGCG 942
|||||
799 GGTATGGAAGTGCCTGTGACAGCCCTTCTCGAGGAGCAAGCTGCGCTTACCTGCG 858
|||||
943 GGAGCTCATCTCGGCCCTCGAGTACTTGCACCTGCCAGAAAGATCGTCCACAGGGACATCAA 1002
|||||
859 GGAGCTCATCTCGGCCCTCGAGTACTTGCACCTGCCAGAAAGATCGTCCACAGGGACATCAA 918
|||||
1003 GCCATCCAACTCTCTCGGGGATGATGGGCACTGGAAGATGCGCGACTTTGGGCTCAG 1062
|||||
919 GCCATCCAACTCTCTCGGGGATGATGGGCACTGGAAGATGCGCGACTTTGGGCTCAG 978
|||||
1063 CAACCGTTTCAAGGGGACAGCGCTCAGCTCTCAGACACGGCGGGAACCCACAGATTTCAT 1122
|||||
979 CAACCGTTTCAAGGGGACAGCGCTCAGCTCTCAGACACGGCGGGAACCCACAGATTTCAT 1038
|||||
1123 GGCCCCCGAGGCCATTTCTGATTCGGCCAGAGCTTTCAGTGGGAAGGCTTGGATGTATG 1182
|||||
1039 GGCCCCCGAGGCCATTTCTGATTCGGCCAGAGCTTTCAGTGGGAAGGCTTGGATGTATG 1098
|||||
1183 GGCCACTGGGCTCAGTTGTATCTGCTTTGTATGGGAAGTGGCCATTCATCGACGATTT 1242
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1099 GGCCACTGGGCTCAGTTGTATCTGCTTTGTATGGGAAGTGGCCGTTTCATCGACGATTT 1158
|||||
1243 CATCTGGCCCTCCACAGGAGATCAAGAATGAGCCGCTGTGTTCTCTGAGGAGCCAGA 1302
|||||
1159 CATCTGGCCCTCCACAGGAGATCAAGAATGAGCCGCTGTGTTCTCTGAGGAGCCAGA 1218
|||||
1303 AATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAAATCCCGAGACGAG 1362
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1219 AATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAAATCCCGAGACGAG 1278
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1363 AATTGGGCTGACGACATCAAGTTGCACCTTGGTGACCAAGAAACGGGGAGAGCCCT 1422
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1279 AATTGGGCTGACGACATCAAGTTGTCACCTTGGGTGACCAAGAAACGGGGAGAGCCCT 1338
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1423 TCCTTCGAGGAGGAGCACTGACAGCTGTGAGTGACAGAGGGGAGGTTTAAGAATC 1482
|||||
1339 TCCTTCGAGGAGGAGCACTGACAGCTGTGAGTGAGTGACAGAGGAGGTTTAAGAATC 1398
|||||
1483 AGTCAGGCTCATCCCGAGCTGACACCAAGTTCATCTGTTGAAGTCCATGCTGAGGAAGCG 1542
|||||
1399 AGTCAGGCTCATCCCGAGCTGACACCAAGTTCATCTGTTGAAGTCCATGCTGAGGAAGCG 1458
|||||
1543 TTCTTTTGGAAACCCGTTTGAAGGAGGTTTGGTGAAGGGGCAAGAGCGATCATCTCTGCTCC 1602
|||||
1459 TTCTTTTGGAAACCCGTTTGAAGGAGGTTTGGTGAAGGGGCAAGAGCGATCATCTCTGCTCC 1518
|||||
1603 AGGAAACCTTACTGTGTGAAGAGGTTTGGTGAAGGGGCAAGAGCGATCATCTCTGCTCC 1662
|||||
1519 AGGAAACCTTACTGTGTGAAGAGGTTTGGTGAAGGGGCAAGAGCGATCATCTCTGCTCC 1578
|||||
1663 CGTCAGGAAGACGAGGCTGCATCTCTGAGCCCTGCATGACCCAGGGCCACCCGGCAGC 1722
|||||

Db 1579 CGTCCAGGAAGACGAGGCTGCTCCTCAGCCCTGTCATGACCCAGGCGCCACCCCGGACG 1638
Qy 1723 ACATCTATCCCGCGCTTCGAGAGCCCAACCCCTCATCAACAGACGCGCCCGGAGGAGG 1782
Db 1639 ACATCTATCCCGCGCTTCGAGAGCCCAACCCCTCATCAACAGACGCGCCCGGAGGAGG 1698
Qy 1783 GGGCTGGGACTGACAGCCCACTCCCGCCCTCCCCCATCGTGTGATGACCTTCCAGCG 1842
Db 1699 GGGCTGGGACTGACAGCCCACTCCCGCCCTCCCCCATCGTGTGATGACCTTCCAGCG 1758
Qy 1843 ACGCAGCTCCAGGACAGACTGGAAATGATGTCAATTTGGGGTCTTGGGGGAGGCTCC 1902
Db 1759 ACGCAGCTCCAGGACAGACTGGAAATGATGTCAATTTGGGGTCTTGGGGGAGGCTCC 1818
Qy 1903 ACGAGGCACTCTCTCTTTGSCCCTCTTGGCCTGACCCATTCCTGTGGGGAAACCGG 1962
Db 1819 ACGAGGCACTCTCTCTTTGACCTCTTGGACCTTCTTGGCCTGACCCATTCCTGTGGGGAAACCGG 1878
Qy 1963 GTGCCATGGAGCTCAAGAAATGCCAGCCGCTGTTGGCATGGCTTGGGGCAGAGGCA 2022
Db 1879 GTGCCATGGAGCTCAAGAAATGCCAGCCGCTGTTGGCATGGCTTGGGGCAGAGGCA 1938
Qy 2023 GAGCAGAGACCAAGATGGCAGGTGAGGCGCAGCTTACCAACAGGAAGAGACTCC 2082
Db 1939 GAGCAGAGACCAAGATGGCAGGTGAGGCGCAGCTTACCAACAGGAAGAGACTCC 1998
Qy 2083 GCTGGGCGCGGCGAGGCTGCTCAGCTGCCACAGCATATGTGGAGAGGGGCTACCC 2142
Db 1999 GCTGGGCGCGGCGAGGCTGCTCAGCTGCCACAGCATATGTGGAGAGGGGCTACCC 2058
Qy 2143 TGCCCACTTGGGGTGGTGCCACAGAGCTCTTGTCTATTTCAGACGCT 2190
Db 2059 TGCCCACTTGGGGTGGTGCCACAGAGCTCTTGTCTATTTCAGAGCT 2106
RESULT 3
AAD30566
ID AAD30566 standard; cDNA; 1937 BP.
XX AAD30566;
XX
XX 21-MAY-2002 (first entry)
XX Human kinase polypeptide (PKIN-19) cDNA.
XX
XX Human; kinase polypeptide; PKIN-19; gene therapy; Addison's disease;
KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
KW cholestasis; cardiac; cardiovascular disorder; Niemann-Pick's disease;
KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
KW drug screening; transgenic animal; antiinflammatory; hepatotropic;
KW hypotensive; anti-HIV; enzyme; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 65..1582
FT /*tag= a
FT /product= "Human PKIN-19"
XX
XX WO200208399-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US023092.
XX
XX 21-JUL-2000; 2000US-0220038P.
PR 28-JUL-2000; 2000US-0222112P.
PR 04-AUG-2000; 2000US-0222831P.
PR 11-AUG-2000; 2000US-0224729P.
XX

PA	(INCY-) INCYTE GENOMICS INC.	Db	382	GCCCAACATCGAGTCCCAACACGTCGCCATCTCAGATGCAGAGCACTGCTGCAGCTGAA	441
PA	(THOR/) THORNTON M.	QY	550	CCAGTACAAAGTCGACAGTGCAGATTGGCAAGGGTGCTACGGTGTGCTGAGGCTGGCCTA	609
PI	Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK;	Db	442	CCAGTACAAAGTCGACAGTGCAGATTGGCAAGGGTGCTACGGTGTGCTGAGGCTGGCCTA	501
PI	Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;	QY	610	CAACGAAAGTGAAGACAGACATATGCAATGAAAGTCTTTCACAAAAGAAAGTTACTGAA	669
PI	Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;	Db	502	CAACGAAAGTGAAGACAGACATATGCAATGAAAGTCTTTCACAAAAGAAAGTTACTGAA	561
PI	Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;	QY	670	GCAGTATGCTTTTCCAGTGCCTCCCGGAGAGGGTCCAGGCTGCCAGGAGGACC	729
PI	Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;	Db	562	GCAGTATGCTTTTCCAGTGCCTCCCGGAGAGGGTCCAGGCTGCCAGGAGGACC	621
DR	WPI; 2002-206083/26.	QY	730	AGCCAAAGCAGCTGCTGCCCTCGAGCGGGTGTACACAGAGATTGCCATCTCTGAAGAAGCT	789
DR	P-PSDB; AAEL19161.	Db	622	AGCCAAAGCAGCTGCTGCCCTCGAGCGGGTGTACACAGAGATTGCCATCTCTGAAGAAGCT	681
XX	New human kinase polypeptide, useful in diagnosis, prevention and	QY	790	GGACACGCTGAATGTGGTCAAACTGATCGAGGTCTGGATGACCCAGCTGAGGACAACTT	849
XX	treatment of cancer, immune disorder, growth and developmental disorder,	Db	682	GGACACGCTGAATGTGGTCAAACTGATCGAGGTCTGGATGACCCAGCTGAGGACAACTT	741
PT	cardiovascular disorder and lipid disorder.	QY	850	CTATTTGGTGTGACCTCTCGAGAAAGGGCCCGTCTATGGAAGTGCCTGTGACAGGCC	909
XX	Claim 5; Page 193-194; 196pp; English.	Db	742	CTATTTGGTGTGACCTCTCGAGAAAGGGCCCGTCTATGGAAGTGCCTGTGACAGGCC	801
CC	The present invention relates to an isolated human kinase polypeptide	QY	910	CTTCTCGAGGAGCAAGCTGCGCTCTTACCTGCGGAGCGTCTATCTGGGCTCGAGTACTT	969
CC	(PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is	Db	802	CTTCTCGAGGAGCAAGCTGCGCTCTTACCTGCGGAGCGTCTATCTGGGCTCGAGTACTT	861
CC	useful for diagnosing, treating and preventing cancer (e.g., leukaemia,	QY	970	GCATGCCAGAGATGCTCCACAGGACATCAAGCCATCAACCTGCTCTCGGGGATGA	1029
CC	lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency	Db	862	GCATGCCAGAGATGCTCCACAGGACATCAAGCCATCAACCTGCTCTCGGGGATGA	921
CC	syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's	QY	1030	TGCGCAGCTGAAGTCGCGCTTTGGCGTCAGCACACAGTCTTGAGGGGAAACAGCTCA	1089
CC	disease, rheumatoid arthritis), a growth and developmental disorder (e.g.	Db	922	TGCGCAGCTGAAGTCGCGCTTTGGCGTCAGCACACAGTCTTGAGGGGAAACAGCTCA	981
CC	buritis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a	QY	1090	GCTGTCCAGCACGGGGAAACCCAGCATTCATGCGCCCGGAGGCCATTTCTGATTCGCG	1149
CC	cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial	Db	982	GCTGTCCAGCACGGGGAAACCCAGCATTCATGCGCCCGGAGGCCATTTCTGATTCGCG	1041
CC	infarction), and a lipid disorder (e.g., fatty liver, cholestasis,	QY	1150	CCAGAGCTTCAGTGGGAGGCTTGGATGTATGGGCACTGCGGCTCACTGCTGCTT	1209
CC	Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of	Db	1042	CCAGAGCTTCAGTGGGAGGCTTGGATGTATGGGCACTGCGGCTCACTGCTGCTT	1101
CC	drug screening techniques and to analyse the proteome of a tissue or cell	QY	1210	TGCTATGGAAGTGCCTTTCATCGAGTTCATCTGCGCCCTCCACAGAGAGTCAA	1269
CC	type. PKIN is useful for creating knockin humanised animals or transgenic	Db	1102	TGCTATGGAAGTGCCTTTCATCGAGTTCATCTGCGCCCTCCACAGAGAGTCAA	1161
CC	animals to model human diseases, in somatic or germline gene therapy, to	QY	1270	GAATGAGCCGCTGCTGCTTCTTCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGAT	1329
CC	generate a transcript image of a tissue or cell type, for detecting	Db	1162	GAATGAGCCGCTGCTGCTTCTTCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGAT	1221
CC	differences in the chromosomal location due to translocation, inversion,	QY	1330	CCTGAAGATGTTAGACAGAGATCCCGACAGAGATTTGGGGTGCCAGACATCAAGTTGCA	1389
CC	etc., among normal, carrier or affected individuals, and as hybridisation	Db	1222	CCTGAAGATGTTAGACAGAGATCCCGACAGAGATTTGGGGTGCCAGACATCAAGTTGCA	1281
CC	probes for mapping naturally occurring genomic sequences. PKIN is useful	QY	1390	CCCTTGGGTGACCAAGAACGGGGAGGAGCCCTTCTTCTGCGGAGGAGGACCTGCGAGCT	1449
CC	in southern or northern analysis, dot blot or other membrane-based	Db	1282	CCCTTGGGTGACCAAGAACGGGGAGGAGCCCTTCTTCTGCGGAGGAGGACCTGCGAGCT	1341
CC	technologies, in PCR technologies, in dipstick, pin, multiformat enzyme	QY	1450	GGTGGAGGTGACAGAGGGGGAGGTTTAAAGTCTCAGTCAAGGCTCATCCCCAGCTGACCAAC	1509
CC	linked immunosorbent (ELISA)-like assays and in microarrays utilising	Db	1342	GGTGGAGGTGACAGAGGGGGAGGTTTAAAGTCTCAGTCAAGGCTCATCCCCAGCTGACCAAC	1401
CC	fluids or tissues from patients to detect altered PKIN expression. The	QY	1510	GGTGTATCTCTGGTGAAGTCCATGCTGAGGAAGCTTCTTTGGGAAACCCGCTTTGAGCCCA	1569
CC	present sequence is human PKIN-19 cDNA	Db	1402	GGTGTATCTCTGGTGAAGTCCATGCTGAGGAAGCTTCTTTGGGAAACCCGCTTTGAGCCCA	1461
XX	Sequence 1937 BP; 425 A; 567 C; 603 G; 342 T; 0 U; 0 Other;	QY	1570	GSCACGGAGGAGAGCGATCCATGCTCTGCTCCAGGAACCTTACTGTTGAAGAGGGTT	1629
XX	Query Match 87.1%; Score 1906.4; DB 6; Length 1937;	Db	1462	AGCACGGAGGGAAGAGCGATCCATGCTGCTCCAGGAACCTTACTGTTGAAGAGGGTT	1521
XX	Best Local Similarity 99.7%; Pred. No. 0;				
XX	Matches 1910; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY	130 GTTCCCAACAGGCTACGAGAGAACCCCTTGACTGAAGCAATCGAGGGGGTCCAGC	189			
Db	22 GTTCCCAACAGGCTACGAGAGAACCCCTTGACTGAAGCAATCGAGGGGGTCCAGC	81			
QY	190 TGTCTGCTCCAGGATCTCTCGGCGAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTGAC	249			
Db	82 TGTCTGCTCCAGGATCTCTCGGCGAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTGAC	141			
QY	250 TCACCTGGAGGAGGAGATGCTGCGCCAGAGCTTACTAGAAACGGTGTGGACCCGCCACC	309			
Db	142 TCACCTGGAGGAGGAGATGCTGCGCCAGAGCTTACTAGAAACGGTGTGGACCCGCCACC	201			
QY	310 ACGGGCCAGAGTCCCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCC	369			
Db	202 ACGGGCCAGAGTCCCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCC	261			
QY	370 TAGCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGCAGGAAGCTATCTGAGGC	429			
Db	262 TAGCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGCAGGAAGCTATCTGAGGC	321			
QY	430 GCAGGCTGGGCTTATGCCACGGGGCTTCCAGCCACATCTCTCCCGCGGCTGCGGAG	489			
Db	322 GCAGGCTGGGCTTATGCCACGGGGCTTCCAGCCACATCTCTCCCGCGGCTGCGGAG	381			
QY	490 GCCCACCATCGAGTCCACACGCTGCGCCATCTCAGATGCAGAGGACTGGTGCAGCTGAA	549			

QY 1630 TGGTGAAGGGGCAAGAGCCAGAGCTCCCGGGCTCCAGAGAGAGAGAGCTGATCTG 1689
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1522 TGGTGAAGGGGCAAGAGCCAGAGCTCCCGGGCTCCAGAGAGAGAGAGCTGATCTG 1581
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1690 AGCCCTGCTATGACCCAGAGGCGACCCGGCAGACACACTCATCCCGCGCTCCAGAGGCC 1749
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1582 AGCCCTGCTATGACCCAGAGGCGACCCGGCAGACACACTCATCCCGCGCTCCAGAGGCC 1641
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1750 ACCCTCATGCAACAGAGCCCGCCCGCAGAGGCGGCTGGGGACTGAGAGCCCACTCCCG 1809
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1642 ACCCTCATGCAACAGAGCCCGCCCGCAGAGGCGGCTGGGGACTGAGAGCCCACTCCCG 1701
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1810 CCCTCCCATGCTGCTGATGATGCTCCAGGACGACGACGCTCCAGGACAGACTGGATG 1869
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1702 CCCTCCCATGCTGCTGATGATGCTCCAGGACGACGACGCTCCAGGACAGACTGGATG 1761
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1870 TATGTCATTTGGGCTTTGGGGGAGGGCTCCACAGAGGCGCATCTCTCTTTCTTTGGGCC 1929
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1762 TATGTCATTTGGGCTTTGGGGGAGGGCTCCACAGAGGCGCATCTCTCTTTCTTTGGGCC 1821
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1930 TCCTTGCGCTGACCATTTCTGTGGGAAACCGGGTGGCCATGAGAGCTCAGAAATGCCAC 1989
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1822 TCCTTGCGCTGACCATTTCTGTGGGAAACCGGGTGGCCATGAGAGCTCAGAAATGCCAC 1881
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1990 CCGGCTGCTGGCTGCTGGGGGAGGGCTCCACAGAGGCGAGAGGACAGGATGGCGAG 2045
 QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1882 CCGGCTGCTGGCTGCTGGGGGAGGGCTCCACAGAGGCGAGAGGACAGGATGGCGAG 1937

RESULT 4

ID ABK49563

AC ABK49563; standard; DNA; 2711 BP.

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DR P-PSDB; AAU79458.

XX New human transferase protein for diagnosing and treating disorders e.g.
 PT cancer, Alzheimer's disease, anorexia, diabetes and to identify
 modulators for therapeutic use.
 XX
 PS
 XX Claim 1; Fig 16; 143pp; English.

CC The invention relates to an isolated human kinase polypeptide encoded by
 the DNAs designated 1658, 1423 and 16002 including fragments,
 CC homologues and allelic variants. Also included are a host cell comprising
 CC the DNA, an antibody which selectively binds to the novel kinase, a
 CC method for producing the novel kinase comprising culturing the host cell
 CC and recovering the protein, detecting the presence of the DNA in a sample
 CC comprising contacting the sample with a compound which selectively
 CC hybridises to the DNA and determining whether the compound has bound and
 CC identifying compounds which bind to and/or modulate the protein
 CC comprising contacting the protein with a test compound and determining
 CC whether the compound has bound to and/or modulated the function of the
 CC protein (the modulators may be a small molecule, a peptide, a
 CC phosphopeptide, an antibody or a fragment of the full length protein).
 CC The nucleic acids, proteins, identified modulators and antibodies are
 CC useful in the diagnosis, monitoring and treatment of a wide range of
 CC diseases and disorders (many examples of which are listed in the
 CC specification) including cellular proliferative disorders (e.g. cancers
 CC of the lung and breast, carcinomas, tumours, adenocarcinomas,
 CC haematopoietic neoplastic disorders e.g. leukaemias and lymphomas), brain
 CC and nerve tissue disorders (e.g. cerebral ischaemia, infections such as
 CC meningitis, brain abscess, acquired immunodeficiency syndrome (AIDS) -
 CC disease, Huntington's disease and motor neurone disease) metabolic
 CC disorders (e.g. obesity, anorexia nervosa and diabetes) pain disorders
 CC (e.g. associated with infection, inflammation ischaemia, irritable bowel
 CC syndrome), heart disorders (e.g. myocardial infarction), blood vessel
 CC disorders (e.g. atherosclerosis), disorders of bone metabolism (e.g.
 CC osteoporosis) and haematopoietic disorders (e.g. arthritis). The present
 CC sequence encodes novel human kinase 16002

XX Sequence 2711 BP; 592 A; 752 C; 848 G; 508 T; 0 U; 11 Other;

Query Match 74.7%; Score 1636.2; DB 6; Length 2711;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1652; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 8 GGGCTGAGCTCGGCGATCTGGGCCCCAGCGAGCGGCTGGGGCGGGCGGGCGGGCGGG 67

Db 34 GGGCTGAGCTCGGCGATCTGGGCCCCAGCGAGCGGCTGGGGCGGGCGGGCGGGCGGG 93

QY 68 GCGCGCAGCAGGAGCGAGTGGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 127

Db 94 GCGCGCAGCAGGAGCGAGTGGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 152

QY 128 AGTTTCCCAACAGGCTACCGGAGAACCCCTTGACTGAGCAATGGAGGGGGTCCA 187

Db 153 AGTTTCCCAACAGGCTACCGGAGAACCCCTTGACTGAGCAATGGAGGGGGTCCA 212

QY 188 GCTGTGCTGCCAGGATCCCTCGGCGAGAGCTGGTAGAACCGGTGGCAGCCATCGATGTG 247

Db 213 GCTGTGCTGCCAGGATCCCTCGGCGAGAGCTGGTAGAACCGGTGGCAGCCATCGATGTG 272

QY 248 ACTCATTGGAGAGGAGAGATGGTGGGCCAGAGCCTACTAGAAACGGTGTGGAGCCCCCA 307

Db 273 ACTCATTGGAGAGGAGAGATGGTGGGCCAGAGCCTACTAGAAACGGTGTGGAGCCCCCA 332

QY 308 CCAGGGCCAGAGCTGCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGAGCCGG 367

Db 333 CCAGGGCCAGAGCTGCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGAGCCGG 392

QY 368 CCTAGCCTCTCAGCCAGGAAGCTTTTCCCTACAGGAGCGGGCAGCAGGAAGTATCTGGAG 427

Db 393 CCTAGCCTCTCAGCCAGGAAGCTTTTCCCTACAGGAGCGGGCAGCAGGAAGTATCTGGAG 452

QY 428 GCGCAGGCTGGGCTTATGCCCACGGGGCTGCCAGCCACATCTCCCCCGGGCGGGCGG 487

Human; ss; gene; 16002; kinase; cellular proliferative disorder; cancer;
 carcinoma; tumour; adenocarcinoma; haematopoietic neoplastic disorder;
 leukaemia; lymphoma; brain disorder; cerebral ischaemia; infection;
 meningitis; brain abscess; acquire immunodeficiency syndrome; obesity;
 AIDS-related myopathy; prion disease; Alzheimer's disease; diabetes;
 Parkinson's disease; Huntington's disease; motor neurone disease;
 metabolic disorder; anorexia nervosa; pain; inflammation; ischaemia;
 irritable bowel syndrome; heart disorder; myocardial infarction;
 blood vessel disorder; atherosclerosis; bone metabolism disorder;
 osteoporosis; haematopoietic disorder; arthritis.

Homo sapiens.

Key Location/Qualifiers

FT CDS 198..1883

FT /tag= a

FT /product= "Kinase 16002"

FT /note= "This coding sequence (minus the stop codon) is

specifically claimed in claim 1"

WO200220800-A2.

14-MAR-2002.

03-AUG-2001; 2001WO-US024601.

01-SEP-2000; 2000US-0229299P.

(MILL-) MILLENNIUM PHARM INC.

Meyers RA, Silos-Santiago I;

WPI; 2002-351781/38.

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453 GGCAGGCTGGGCTTATGTCACGCGGCTGCGCAGCCATCTCCCGCGGCTGGCGG 512
QY AGSCCCACCATTGAGTCCACACAGTGGCCATCTCAGATGACAGAGACTGCGTGACAGTG 547
Db AGSCCCACCATTGAGTCCACACAGTGGCCATCTCAGATGACAGAGACTGCGTGACAGTG 572
QY AACAGTACAGCTGACAGTGAATGGCAAGGTCCTACCGTGTTGGTGAAGCTGGCC 607
Db AACAGTACAGCTGACAGTGAATGGCAAGGTCCTACCGTGTTGGTGAAGCTGGCC 632
QY TACAACGAAGTGAAGACACACTATGCAATGAAGTCTTCCCAAAAGAGTACTG 667
Db TACAACGAAGTGAAGACACACTATGCAATGAAGTCTTCCCAAAAGAGTACTG 692
QY AAGCAGTATGGCTTTCCACGTCGCCCTCCCGCAGAGGGTCCCGAGGAGGA 727
Db AAGCAGTATGGCTTTCCACGTCGCCCTCCCGCAGAGGGTCCCGAGGAGGA 752
QY CCAGCCAAAGAGTGTGCTGCGGCTGGAGCGGGTGTACAGAGAGATTGCTTCTGAAGAG 787
Db CCAGCCAAAGAGTGTGCTGCGGCTGGAGCGGGTGTACAGAGAGATTGCTTCTGAAGAG 812
QY CTGGACACGTGAATGTGGTCAAACTGATCGAGGTCTGATGACCCAGTGAAGCAAC 847
Db CTGGACACGTGAATGTGGTCAAACTGATCGAGGTCTGATGACCCAGTGAAGCAAC 872
QY CTCTATTTGGTGTGTTGACCTCTCTGAGAAAGGGGCGCTCATGGAAGTGCCTGTGACAAG 907
Db CTCTATTTGGTGTGTTGACCTCTCTGAGAAAGGGGCGCTCATGGAAGTGCCTGTGACAAG 932
QY CCGTCTCCGAGGAGCAAGTGCCTCTACCTCGGGGAGCTCATCTGGGCTCTGAGTAC 967
Db CCGTCTCCGAGGAGCAAGTGCCTCTACCTCGGGGAGCTCATCTGGGCTCTGAGTAC 992
QY TTGCACTGCGAGAAGATGTCACAGGACATCAAGCAATCCAACTGCTCTGGGGGAT 1027
Db TTGCACTGCGAGAAGATGTCACAGGACATCAAGCAATCCAACTGCTCTGGGGGAT 1052
QY GATGGCAGCTGAAGATCGCGGCTTTGGCGTCAGCAACCAAGTTTCAGGGGAAACGAGCT 1087
Db GATGGCAGCTGAAGATCGCGGCTTTGGCGTCAGCAACCAAGTTTCAGGGGAAACGAGCT 1112
QY CAGCTGTCAGCACGCGGGGAAACCCAGCATTCATGGCCCGGAGCCATTTCTGATTC 1147
Db CAGCTGTCAGCACGCGGGGAAACCCAGCATTCATGGCCCGGAGCCATTTCTGATTC 1172
QY GGCAGAGCTTCAGTGGGAGGCTTTGGATGATGAGGCGCACTGGCGTCACTGTTACTGC 1207
Db GGCAGAGCTTCAGTGGGAGGCTTTGGATGATGAGGCGCACTGGCGTCACTGTTACTGC 1232
QY TTGTCTATGGGAAGTGGCCATTCATCGAGATTTTCATCTGGCCCTCCACAGGAGATC 1267
Db TTGTCTATGGGAAGTGGCCATTCATCGAGATTTTCATCTGGCCCTCCACAGGAGATC 1292
QY AAGATGACCCGTGTGTTCTTCTAGGAGCGAGAAATCAGCGAGAGCTCAAGGACCTG 1327
Db AAGATGACCCGTGTGTTCTTCTAGGAGCGAGAAATCAGCGAGAGCTCAAGGACCTG 1352
QY ATCTCAAGATTTAGACAGATCCGAGACGAGAAATTTGGGTGCGGACATCAAGTTG 1387
Db ATCTCAAGATTTAGACAGATCCGAGACGAGAAATTTGGGTGCGGACATCAAGTTG 1412
QY CACCTTTGGGTGACCAAGAACGGGAGGAGCCCTTCTTTCGAGAGGAGCACTCAGC 1447
Db CACCTTTGGGTGACCAAGAACGGGAGGAGCCCTTCTTTCGAGAGGAGCACTCAGC 1472
QY GTGGTGGAGTGAACAGGGGAGGTTAAGAACTCAGTCAAGTCAATCCCGAGTGGAC 1507
Db GTGGTGGAGTGAACAGGGGAGGTTAAGAACTCAGTCAAGTCAATCCCGAGTGGAC 1532
QY ACGGTGATCTGTTGAAGTCCATGCTGAGGAGCGTTCTTTGGGAACCGGTTGAGCC 1567
|||||

Db 1533 ACGGTGATCTGTTGAAGTCCATGCTGAGGAAGCGTTCTCTTTGGGAACCCGTTTGAGCCC 1592
QY CAGGCAAGGAGGAGGAGGATCCATGTTCTGCTCCAGGAACCTACTGTTGAAAGAGGG 1627
Db CAGGCAAGGAGGAGGAGGATCCATGTTCTGCTCCAGGAACCTACTGTTGAAAGAGGG 1652
QY TTTGGTGAAGGGGGCAAGAGCCAGAGTCCCGCGGTCCAGGAACGA 1677
Db TTTGGTGAAGGGGGCAAGAGCCAGAGTCCCGCGGTCCAGGCTTACCA 1702
RESULT 5
ABZ11551
ID ABZ11551 standard; cDNA; 2018 BP.
XX
AC ABZ11551;
XX
DT 20-JAN-2003 (first entry)
XX
XX Human polynucleotide SEQ ID NO 433.
DE
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI: 2002-759812/82.
DR P-PSDB; ABP69334.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
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PS Claim 1; SEQ ID NO 433; 1012pp + Sequence Listing; English.
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CC The invention relates to an isolated polynucleotide (1) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 2018 BP; 453 A; 600 C; 603 G; 362 T; 0 U; 0 Other;
Query Match 73.5%; Score 1610.2; DB 6; Length 2018;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 28; Indels 1; Gaps 1;
129 GGTTCCTCAACAGGCTACGAGAGAACCCCTTGTGACTGAGCAATAGAGGGGGGTCCAG 188
188 GGTTCCTCAACAGGCTACGAGAGAACCCCTTGTGACTGAGCAATAGAGGGGGGTCCAG 247
189 CTGTCTGTGTCAGGATCTCTCGGCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTGA 248
248 CTGTCTGTGTCAGGATCTCTCGGCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTGA 307
249 CTCACTTTGGAGGAGCGAGATGGTGGCCCGCAGAGCCCTACTAGAAACGGTGTGAGCCGCCAC 308
308 CTCACTTTGGAGGAGCGAGATGGTGGCCCGCAGAGCCCTACTAGAAACGGTGTGAGCCGCCAC 367
309 CACGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCACGCCGGC 368
368 CACGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCACGCCGGC 427
369 CTAGCCTCTCAGCCAGGAGCTTTTCCCTACAGGAGCGGCCAGAGGAGCTATCTGGAGG 428
428 CTAGCCTCTCAGCCAGGAGCTTTTCCCTACAGGAGCGGCCAGAGGAGCTATCTGGAGG 487
429 CGTAGGCTGGGCTTATGCGACGGGGCTGCGACGCAATCTCCCGCGGCGCTGGCGGA 488
488 CGTAGGCTGGGCTTATGCGACGGGGCTGCGACGCAATCTCCCGCGGCGCTGGCGGA 547
489 GGCCCAACCATCAGTCCACACAGTGGCCATCTCAGATGACAGAGACTGCGTGCAGCTGA 548
548 GGCCCAACCATCAGTCCACACAGTGGCCATCTCAGATGACAGAGACTGCGTGCAGCTGA 607
549 ACCAGTACAAGCTGCAGAGTGGCAAGGGGTGCTACCGTGTGTGTGAGGCTGGCCT 608
608 ACCAGTACAAGCTGCAGAGTGGCAAGGGGTGCTACCGTGTGTGTGAGGCTGGCCT 667
609 ACAAGAAAGTGAAGACAGACATATGCAATGAAGTCCCTTCCAAAAGAAAGTACTGA 668
668 ACAAGAAAGTGAAGACAGACATATGCAATGAAGTCCCTTCCAAAAGAAAGTACTGA 727
669 AGCAGTATGGCTTTCCAGTGGCTCCCGAGAGGGTCCAGGCTCCCGAGGAGGAC 728
728 AGCAGTATGGCTTTCCAGTGGCTCCCGAGAGGGTCCAGGCTCCCGAGGAGGAC 787
729 CAGCCAAAGCTGCTGCCCTCGAGCGGGTGTACAGGAGATGCCATCTCTGAAGAAGC 788
788 CAGCCAAAGCTGCTGCCCTCGAGCGGGTGTACAGGAGATGCCATCTCTGAAGAAGC 847
789 TGGACCAAGTGAATGTGTGCTAACTGATCGAGGTCTGTGATGACCCAGCTGAGGACACC 848
848 TGGACCAAGTGAATGTGTGCTAACTGATCGAGGTCTGTGATGACCCAGCTGAGGACACC 907
849 TCTATTTGGTGTGTTGACCTCTGAGAAAGGGCCCGCTCATGGAAGTGCCTGTGACAAGC 908
908 TCTATTTGGTGTGTTGACCTCTGAGAAAGGGCCCGCTCATGGAAGTGCCTGTGACAAGC 967
909 CTTTCTCGGAGAGCAAGCTCGCTCTACTCTGCGGAGCGTCACTCTGGGCTTCGAGTACT 968
968 CTTTCTCGGAGAGCAAGCTCGCTCTACTCTGCGGAGCGTCACTCTGGGCTTCGAGTACT 1027
969 TGCATGCGCAGAGATCTGCACAGGGACATCAAGCCATCAACCTGCTCTCTGGGGATG 1028
1028 TGCATGCGCAGAGATCTGCACAGGGACATCAAGCCATCAACCTGCTCTCTGGGGATG 1087
1029 ATGGCAGCTGAAGATCGCGCACTTTGGCGTTCAGCAACACAGTTTGGAGGGAACGCGCTC 1088
1088 ATGGCAGCTGAAGATCGCGCACTTTGGCGTTCAGCAACACAGTTTGGAGGGAACGCGCTC 1147
1089 AGCTGTCAGACGCGGGGAACCCAGAGATTCTATGGCCCGCGAGGCGATTTCTGATTCG 1148
1148 AGCTGTCAGACGCGGGGAACCCAGAGATTCTATGGCCCGCGAGGCGATTTCTGATTCG 1207

QY GCCAGAGCTTCAGTGGGAAGCCCTTGGATGTATGGCCACTGGCGTCACGTTTACTGCT 1208
DB GCCAGAGCTTCAGTGGGAAGCCCTTGGATGTATGGCCACTGGCGTCACGTTTACTGCT 1267
QY TTGTCTATGGGAAGTGCCTTTCATCGACGATTTTCATCTTGGCCCTCCACAGGAAGATCA 1268
DB TTGTCTATGGGAAGTGCCTTTCATCGACGATTTTCATCTTGGCCCTCCATAGGAAGATCA 1327
QY AGAATGAGCCCGTGTGTTCTTGAGAGCCGAAATCAGGAGGAGCTCAAGACCTGA 1328
DB AGAATGAGCCCGTGTGTTCTTGAGAGCCGAAATCAGGAGGAGCTCAAGACCTGA 1387
QY TCCTGAGAGTCTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTGC 1388
DB TCCTGAGAGTCTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTGC 1447
QY ACCCTTGGGTGACCAAGAACGGGAGAGGCCCTTCTTCGGAGGAGGAGCACTGCAGCG 1448
DB ACCCTTGGGTGACCAAGAACGGGAGAGGCCCTTCTTCGGAGGAGGAGCACTGCAGCG 1507
QY TGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCA 1508
DB TGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCA 1567
QY CGGTGATCCTGTTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAAACCCGTTTGAGCCCC 1568
DB CGGTGATCCTGTTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAAACCCGTTTGAGCCCC 1627
QY AGGCACGAGGAGGAAAGAGCGATCCATGTCTGCCAGGAAACCTACTGGTGAAGAAAGGCT 1628
DB AAGCACGAGGAGGAAAGAGCGATCCATGTCTGCCAGGAAACCTACTGGTGAAGAAAGGCT 1687
QY TTGTGAAGGGGGCAAGAGCCAGAGCTCCCGCGGTCAGGAAGAGGAGCTGCATCCT 1688
DB TTGTGAAGGGGGCAAGAGCCAGAGCTCCCGCGGTCAGGAAGAGGAGCTGCATCCT 1747
QY GAGCCCTGTCATGACACCGAGGCCACCGCGCAGCACACTCATCCGCGCTCCAGAGGCC 1748
DB GAGCCCTGTCATGACACCGCAACCGCAACCGCGCAGCACACTCATCCGCGCTCCAGAGGCC 1806
QY CACCCCTCATGCAACAGCGCCCGCCGAGGAGCGGGGCTGGGAGCTG 1795
DB CCCACCCCTCAATCAACAGCGCCCGCCGCAAGCGCCAGGGGGGCTG 1853

RESULT 6

ABX97035

ID ABX97035 standard; cDNA; 1611 BP.

AC ABX97035;

XX ABX97035;

DT 20-MAY-2003 (first entry)

XX Human NOV15b cDNA.

DE NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;

KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KW human; gene; ss.

OS Homo sapiens.

XX WO200272757-A2.

PN 19-SEP-2002.

XX 08-MAR-2002; 2002MO-US006908.

XX 08-MAR-2001; 2001US-0274101P.

XX 08-MAR-2001; 2001US-0274194P.

XX 08-MAR-2001; 2001US-0274281P.

XX 08-MAR-2001; 2001US-0274322P.

XX 09-MAR-2001; 2001US-0274849P.

PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 21-MAR-2001; 2001US-0277327P.
PR 22-MAR-2001; 2001US-0277791P.
PR 23-MAR-2001; 2001US-0277833P.
PR 26-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 03-APR-2001; 2001US-0281194P.
PR 14-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX
PA (CURA-) CURAGEN CORP.
PI Padigar M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
PI Zernusen B, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangoli E, Vernet CAM, Guo X, Tcherniev V;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
PI Lepley DM, Rieger DK;
XX WPI; 2002-723332/78.
DR P-PSDB; ABU65068.
XX
PT NOVX polypeptides and polynucleotides, useful for preventing or treating
a disorder associated with aberrant NOVX expression or activity e.g.,

cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.
Claim 13; Page 139; 1103pp; English.
This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-ABX97593. ABX97008-ABX97185 encode the NOVX proteins described in ABU65041-ABU65218
Sequence 1611 BP; 366 A; 461 C; 497 G; 287 T; 0 U; 0 Other;
Query Match 73.1%; Score 1601.4; DB 6; Length 1611;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 122 GCGCCAGGTTCCCAACAGGCTACGCACAGAACCCCTTGACTGAAGCAATGGAGGG 181
DB 1 GCGCCAGGTTCCCAACAGGCTACGCACAGAACCCCTTGACTGAAGCAATGGAGGG 60
QY 182 GGTCCAGCTGTCTGCTGCCAGGATCCTCGGCAGAGCTGTGTAACCGGTGGCAGGCATC 241
DB 61 GGTCCAGCTGTCTGCTGCCAGGATCCTCGGCAGAGCTGTGTAACCGGTGGCAGGCATC 120
QY 242 GATGTGACTCACTTGGAGGAGGCAGATGTTGGCCAGAGCCTACTAGAACCGTGTGGAC 301
DB 121 GATGTGACTCACTTGGAGGAGGCAGATGTTGGCCAGAGCCTACTAGAACCGTGTGGAC 180
QY 302 CCCCCACACGCGGCCAGAGCTGCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCCA 361
DB 181 CCCCCACACGCGGCCAGAGCTGCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCCA 240
QY 362 GCGCGGCTTAGCTCTCAGCCAGGAAGCTTCCCTACAGGAGCGGCCAGCAGAGCTAT 421
DB 241 GCGCGGCTTAGCTCTCAGCCAGGAAGCTTCCCTACAGGAGCGGCCAGCAGAGCTAT 300
QY 422 CTGGAGGCGCAGGCTGGGCTTTATGCCAGGGGCTGCCAGCCACATCTCCCGCGGGCC 481
DB 301 CTGGAGGCGCAGGCTGGGCTTTATGCCAGGGGCTGCCAGCCACATCTCCCGCGGGCC 360
QY 482 TGGCGGAGGCCACCATCGAGTCCACACGCTGGGCATCTCAGATGCAGAGACTGCGTG 541
DB 361 TGGCGGAGGCCACCATCGAGTCCACACGCTGGGCATCTCAGATGCAGAGACTGCGTG 420
QY 542 CAGCTGAACCCAGTACAAGCTGCAGAGTGAAGTGGCAGGGGTCCCTACGGTGTGGTGGG 601
DB 421 CAGCTGAACCCAGTACAAGCTGCAGAGTGAAGTGGCAGGGGTCCCTACGGTGTGGTGGG 480
QY 602 CTGGCTTACAACGAAGTGAAGACAGACACTATGCAATGAAGTCTTTTCCAAAAGAG 661
DB 481 CTGGCTTACAACGAAGTGAAGACAGACACTATGCAATGAAGTCTTTTCCAAAAGAG 540
QY 662 TTACTGAAGCAGTATGGCTTTTCCAGTGGCTTCCCGGAGGGTCCAGGCTGCCAG 721
DB 541 TTACTGAAGCAGTATGGCTTTTCCAGTGGCTTCCCGGAGGGTCCAGGCTGCCAG 600
QY 722 GGAGCACCAGCAACAGCAGCTGTGCTGCTGGAGGGGTGATCCAGAGATTGCCATCTG 781
DB 601 GGAGCACCAGCAACAGCAGCTGTGCTGCTGGAGGGGTGATCCAGAGATTGCCATCTG 660
QY 782 AAGAGCTGGACCCAGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGACCCAGCTGAG 841
DB 661 AAGAGCTGGACCCAGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGACCCAGCTGAG 720
QY 842 GACAACTCTATTGGTGTGATGCTCTGAGAAAGGGGCGGCTCATGGAAGTGGCTGT 901

Db 721 GACAACTCTATTGTTGTTGACCTCCTGAGAAAGGGCCCGTCATGGAAGTGCCTGT 780
Qy 902 GACAAGCCCTTCTCGAGGAGCAAGCTGCGCTCTTACCTGCGGAGCGTCACTCTGGGCTC 961
Db 781 GACAAGTCTTCTCGAGGAGCAAGCTGCGCTCTTACCTGCGGAGCGTCACTCTGGGCTC 840
Qy 962 GAGTACTTGCATCGCAGAGATCGTCCACAGGACATCAAGCCATCCAACCTGCTCTG 1021
Db 841 GAGTACTTGCATCGCAGAGATCGTCCACAGGACATCAAGCCATCCAACCTGCTCTG 900
Qy 1022 GGGGATGATGGGCAAGTGAAGATCGCCGACCTTGGCGTCAGCAACCAAGTTTGAGGGAA 1081
Db 901 GGGGATGATGGGCAAGTGAAGATCGCCGACCTTGGCGTCAGCAACCAAGTTTGAGGGAA 960
Qy 1082 GACCTCAGCTGTCCAGCAACCGGGGAACCCAGCATTCATGGCCCGGAGGCCATTCT 1141
Db 961 GACGCTCAGCTGTCCAGCAACCGGGGAACCCAGCATTCATGGCCCGGAGGCCATTCT 1020
Qy 1142 GATTCCGSCCAGAGCTTCAGTGGGAAGGCCCTTGGATGTATGGGCCACTTGGCGTCAAGTTG 1201
Db 1021 GATTCCGSCCAGAGCTTCAGTGGGAAGGCCCTTGGATGTATGGGCCACTTGGCGTCAAGTTG 1080
Qy 1202 TACTGCTTTGCTATGGGAAGTGCCTCATTCAGCAATTCATCTGSCCCTCCACAGG 1261
Db 1081 TACTGCTTTGCTATGGGAAGTGCCTCATTCAGCAATTCATCTGSCCCTCCACAGG 1140
Qy 1262 AAGATCAAGATGAGCCGCTGTCTCTGAGGAGCCAGAAATCAGGAGAGCTCAAG 1321
Db 1141 AAGATCAAGATGAGCCGCTGTCTCTGAGGAGCCAGAAATCAGGAGAGCTCAAG 1200
Qy 1322 GACCTGATCTTGAAGTGTAGACAAGAAATCCGAGAGGAGTGGGTCCAGACATC 1381
Db 1201 GACCTGATCTTGAAGTGTAGACAAGAAATCCGAGAGGAGTGGGTCCAGACATC 1260
Qy 1382 AAGTTGCACTTGGGTGACCAAGAAACGGGAGGAGCCCTTCTCTGAGGAGAGCAC 1441
Db 1261 AAGTTGCACTTGGGTGACCAAGAAACGGGAGGAGCCCTTCTCTGAGGAGAGCAC 1320
Qy 1442 TGCAGCTGTGGAGGTACAGAGGGAGGTTAAGAACTCAGTCAGCTCATCCCCAGC 1501
Db 1321 TGCAGCTGTGGAGGTACAGAGGGAGGTTAAGAACTCAGTCAGCTCATCCCCAGC 1380
Qy 1502 TGGACACGGTGATCCTGCTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAACCCGTTT 1561
Db 1381 TGGACACCGTGATCCTGCTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAACCCGTTT 1440
Qy 1562 GAGCCCCAGGCAAGGAGGAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAA 1621
Db 1441 GAGCCCCAAGCAGGAGGAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAA 1500
Qy 1622 GAAGGTTTGTGAGGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGGAGAGAGGCT 1681
Db 1501 GAAGGTTTGTGAGGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGGAGAGAGGCT 1560
Qy 1682 GCATCCTGAGCCCTGCATGACCCAGGCGCAACCCGCGAGACACTCATCC 1732
Db 1561 GCATCCTGAGCCCTGCATGACCCAGGCGCAACCCGCGAGACACTCATCC 1611

RESULT 7

ABX97034

ID ABX97034 standard; cDNA; 1547 BP.

AC ABX97034;

DT 20-MAY-2003 (first entry)

DE Human NOV15a cDNA.

XX NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
XX human; gene; ss.

OS Homo sapiens.
XX WO200272757-A2.
XX 19-SEP-2002.
XX 08-MAR-2002; 2002WO-US006908.
XX 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277391P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 21-NOV-2001; 2001US-0333272P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX (CURA-) CURAGEN CORP.

PR

XX	20-MAY-2003	(first entry)
DT		
XX		
DE	Human NOV15c cDNA.	
XX		
KW	NOVX; cytosstatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;	
KW	hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;	
KW	human; gene; ss.	
XX		
OS	Homo sapiens.	
OS		
XX		
PN	WC0200272757-A2.	
XX		
PD	19-SEP-2002.	
XX		
XX	08-MAR-2002; 2002WO-US006908.	
XX		
PR	08-MAR-2001; 2001US-0274101P.	
PR	08-MAR-2001; 2001US-0274194P.	
PR	08-MAR-2001; 2001US-0274281P.	
PR	08-MAR-2001; 2001US-0274322P.	
PR	09-MAR-2001; 2001US-0274849P.	
PR	12-MAR-2001; 2001US-0275235P.	
PR	13-MAR-2001; 2001US-0275578P.	
PR	13-MAR-2001; 2001US-0275579P.	
PR	13-MAR-2001; 2001US-0275601P.	
PR	14-MAR-2001; 2001US-0276000P.	
PR	16-MAR-2001; 2001US-0276776P.	
PR	19-MAR-2001; 2001US-0276994P.	
PR	20-MAR-2001; 2001US-0277239P.	
PR	20-MAR-2001; 2001US-0277321P.	
PR	20-MAR-2001; 2001US-0277327P.	
PR	21-MAR-2001; 2001US-0277791P.	
PR	22-MAR-2001; 2001US-0277833P.	
PR	23-MAR-2001; 2001US-0278152P.	
PR	26-MAR-2001; 2001US-0278894P.	
PR	27-MAR-2001; 2001US-0278999P.	
PR	27-MAR-2001; 2001US-0279036P.	
PR	28-MAR-2001; 2001US-0279344P.	
PR	30-MAR-2001; 2001US-0277338P.	
PR	30-MAR-2001; 2001US-0279995P.	
PR	30-MAR-2001; 2001US-0280233P.	
PR	02-APR-2001; 2001US-0280802P.	
PR	02-APR-2001; 2001US-0280822P.	
PR	02-APR-2001; 2001US-0280900P.	
PR	04-APR-2001; 2001US-0281194P.	
PR	13-APR-2001; 2001US-0283675P.	
PR	30-APR-2001; 2001US-0287424P.	
PR	02-MAY-2001; 2001US-0288066P.	
PR	03-MAY-2001; 2001US-0288342P.	
PR	03-MAY-2001; 2001US-0288528P.	
PR	15-MAY-2001; 2001US-0291190P.	
PR	16-MAY-2001; 2001US-0291099P.	
PR	16-MAY-2001; 2001US-0291240P.	
PR	30-MAY-2001; 2001US-0294485P.	
PR	31-MAY-2001; 2001US-0294889P.	
PR	31-MAY-2001; 2001US-0294899P.	
PR	18-JUN-2001; 2001US-0299027P.	
PR	19-JUN-2001; 2001US-0299303P.	
PR	19-JUN-2001; 2001US-0299310P.	
PR	10-JUL-2001; 2001US-0304354P.	
PR	21-JUL-2001; 2001US-0309198P.	
PR	16-AUG-2001; 2001US-0312903P.	
PR	10-SEP-2001; 2001US-0318462P.	
PR	12-SEP-2001; 2001US-0318770P.	
PR	27-SEP-2001; 2001US-0325430P.	
PR	27-SEP-2001; 2001US-0325681P.	
PR	18-OCT-2001; 2001US-0330380P.	
PR	31-OCT-2001; 2001US-0335301P.	
PR	14-NOV-2001; 2001US-0332172P.	
PR	14-NOV-2001; 2001US-0332271P.	
PR	14-NOV-2001; 2001US-0332272P.	
PR	14-NOV-2001; 2001US-0333184P.	

QY 542 CAGCTGAACCACTACAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGTGTGGTGG 601
Db 421 CAGCTGAACCACTACAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGTGTGGTGG 480
QY 602 CTGGCCCTACAAACCAAGTGAAGACAGACACTATGCAATGAAGTCTCTTTCCAAAGAG 661
Db 481 CTGGCCCTACAAACCAAGTGAAGACAGACACTATGCAATGAAGTCTCTTTCCAAAGAG 540
QY 662 TTAATGAAGCAGTATGCTTTTCCAGTTCACCTGCGCCCTCCCGAGAGGGTCCAGGCTGCCAG 721
Db 541 TTAATGAAGCAGTATGCTTTTCCAGTTCACCTGCGCCCTCCCGAGAGGGTCCAGGCTGCCAG 600
QY 722 GGAGGACCAAGCAGCTGCTGCGCCCTGGAGGGGTGTACAGAGATTGTCATCTG 781
Db 601 GGAGGACCAAGCAGCTGCTGCGCCCTGGAGGGGTGTACAGAGATTGTCATCTG 660
QY 782 AAGAAGCTGGACCAAGCTGGAATGGGTCAAACTGATCGAGGTCTGTGATGACCCAGCTGAG 841
Db 661 AAGAAGCTGGACCAAGCTGGAATGGGTCAAACTGATCGAGGTCTGTGATGACCCAGCTGAG 720
QY 842 GACAACTCTATTTG----- 856
Db 721 GACAACTCTATTTG----- 780
QY 857 ----- 856
Db 781 ATGCGCAAGTCCCACTCCCTGCTTCCCTCTGAGCAGCAAGACAGTGGATCCAGTGGCT 840
QY 857 -----GTGTTGACCTCTCTGAGAAAGGGCCCGTCTATGAAAGTGCCTCTGACAAG 907
Db 841 GCGCGCTCAGTGTGTTGACCTCTCTGAGAAAGGGCCCGTCTATGAAAGTGCCTCTGACAAG 900
QY 908 CCTTCTCGAGGAGCAAGCTGCGCTCTACTCGGGAGCGTCACTCTGGGCTCTCGAGTAC 967
Db 901 CCTTCTCGAGGAGCAAGCTGCGCTCTACTCGGGAGCGTCACTCTGGGCTCTCGAGTAC 960
QY 968 TTGCACTGCCAGAGATCGTCCACAGGGACATCAAGCCATCCAACTGCTCTCTGGGGAT 1027
Db 961 TTGCACTGCCAGAGATCGTCCACAGGGACATCAAGCCATCCAACTGCTCTCTGGGGAT 1020
QY 1028 GATGGCAGCTGAAGATCGCCGCTTTGGCTCAGCAACCAAGTTTCTGAGGGGAACGACGCT 1087
Db 1021 GATGGCAGCTGAAGATCGCCGCTTTGGCTCAGCAACCAAGTTTCTGAGGGGAACGACGCT 1080
QY 1088 CAGCTTCCAGCAGCGCGGGAACCCAGCAATTCATGCGCCCGCAGGACCAATTTCTGATTC 1147
Db 1081 CAGCTTCCAGCAGCGCGGGAACCCAGCAATTCATGCGCCCGCAGGACCAATTTCTGATTC 1140
QY 1148 GGCCAGCTTCACTGGGAGGCTTGGATGATGGGCCACTGGCGTCAGTTGTACTGC 1207
Db 1141 GGCCAGCTTCACTGGGAGGCTTGGATGATGGGCCACTGGCGTCAGTTGTACTGC 1200
QY 1208 TTTGCTATGGGAAGTGCCTATTCAGCAGATTTCATCTGGCCCTCCACAGGAAGATC 1267
Db 1201 TTTGCTATGGGAAGTGCCTATTCAGCAGATTTCATCTGGCCCTCCACAGGAAGATC 1260
QY 1268 AAGAATGAGCCGTGTGTTTCTGAGGAGCCAGAAATCAGCAGAGCTCAAGGACCTG 1327
Db 1261 AAGAATGAGCCGTGTGTTTCTGAGGAGCCAGAAATCAGCAGAGCTCAAGGACCTG 1320
QY 1328 ATCCTGAAGATTAGACAGATCCGAGACAGATTGGGTGCGCAGACATCAAGTTG 1387
Db 1321 ATCCTGAAGATTAGACAGATCCGAGACAGATTGGGTGCGCAGACATCAAGTTG 1380
QY 1388 CACCTTGGTGTACCAAGACCGGGAGGAGCCCTCTCTTCGAGGAGGAGCACTGACG 1447
Db 1381 CACCTTGGTGTACCAAGACCGGGAGGAGCCCTCTCTTCGAGGAGGAGCACTGACG 1440
QY 1448 GTGGTGAAGTGCAGAGGGGGAGGTTAAGAACTCAGTCAAGCTCATGCCAGCTGAC 1507
Db 1441 GTGGTGAAGTGCAGAGGGGGAGGTTAAGAACTCAGTCAAGCTCATGCCAGCTGAC 1500
QY 1508 ACGTGTATCTGTGTAAGTCCATGCTGAGGAAGCGTTCTTTGGGAACCCGTTTGAGCC 1567

RESULT 9

AAS06710
ID AAS06710 standard; cDNA; 1542 BP.XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
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AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;

RESULT 9

AAS06710
ID AAS06710 standard; cDNA; 1542 BP.XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
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AC AAS06710;XX
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AC AAS06710;XX
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AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;XX
AC AAS06710;

SQ	Sequence	1542 BP; 349 A; 428 C; 483 G; 282 T; 0 U; 0 Other;
Query Match	66.7%; Score 1461.8; DB 4; Length 1542;	
Best Local Similarity	97.9%; Pred. NO. 1.1e-307;	
Matches 1513; Conservative	0; Mismatches 2; Indels 30; Gaps 2;	
QY	173	ATGAGGGGGTCCAGCTGTCTGTCGCCAGGATCCTCGGCAGAGCTGGTAGAGGGGTG 232
DB	1	ATGAGGGGGTCCAGCTGTCTGTCGCCAGGATCCTCGGCAGAGCTGGTAGAGGGGTG 60
QY	233	GCAGCCATCGATGTGACTCACTTGGAGGAGGAGATGGTGGCCACAGACCTACTAGAAAC 292
DB	61	GCAGCCATCGATGTGACTCACTTGGAGGAGGAGATGGTGGCCACAGACCTACTAGAAAC 120
QY	293	GGTGTGACCCCCACACAGGGCCAGAGCTGCTGTGTATGCCCTGGCAGTACTTCAAGA 352
DB	121	GGTGTGACCCCCACACAGGGCCAGAGCTGCTGTGTATGCCCTGGCAGTACTTCAAGA 180
QY	353	CTGCTCCAGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGAGCGGCCAGCA 412
DB	181	CTGCTCCAGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGAGCGGCCAGCA 240
QY	413	GGAAGCTATCTGGAGGCGAGGCTGGGCTTTATGCCACGGGGCTTGGCCAGCCACATCTCC 472
DB	241	GGAAGCTATCTGGAGGCGAGGCTGGGCTTTATGCCACGGGGCTTGGCCAGCCACATCTCC 300
QY	473	CCCCGGGCTGGCGAGGCCACCATCGAGTCCACACAGTGGCCATCTCAGATGCAGAG 532
DB	301	CCCCGGGCTGGCGAGGCCACCATCGAGTCCACACAGTGGCCATCTCAGATGCAGAG 360
QY	533	GACTGCGTGCAGCTGAACCCAGTACAGCTGCAGAGTGAGATTGGCA-----578
DB	361	GACTGCGTGCAGCTGAACCCAGTACAGCTGCAGAGTGAGATTGGCA-----578
QY	579	-----AGGGTCCCTACCGTGTGGTGGCTGGCTTCAACAAAGTGAAGAC 625
DB	421	GATGCTATCTGCAGGGTGCCTTACGGTGTGGTGGCTTCAACAAAGTGAAGAC 480
QY	626	AGACACTATGCAATCAAGTCTTTTCCAAAGAGTTTACTGMAAGCTATGGCTTTCCA 685
DB	481	AGACACTATGCAATCAAGTCTTTTCCAAAGAGTTTACTGMAAGCTATGGCTTTCCA 540
QY	686	CGTCCCTCCCTCCCGGAGGGTCCAGGCTGCCAGGGAGGACCAAGCAGCTGCTG 745
DB	541	CGTCCCTCCCTCCCGGAGGGTCCAGGCTGCCAGGGAGGACCAAGCAGCTGCTG 600
QY	746	CCCTCGAGCGGGTTACAGAGATTCCTGGAAGAGCTGGACACGTAATGTG 805
DB	601	CCCTCGAGCGGGTTACAGAGATTCCTGGAAGAGCTGGACACGTAATGTG 660
QY	806	GTCAACTGATCGAGTCTGGATGACCCAGCTGAGGACACCTCTATTGGTGTTCAC 865
DB	661	GTCAACTGATCGAGTCTGGATGACCCAGCTGAGGACACCTCTATTGGTGTTCAC 717
QY	866	CTCTCTGAGAAAGGGCCCGCTCATGGAAGTGCCTGTGCAAGGCCCTTCTCGAGGAGCAA 925
DB	718	CTCTCTGAGAAAGGGCCCGCTCATGGAAGTGCCTGTGCAAGGCCCTTCTCGAGGAGCAA 777
QY	926	GCTGCGCTCTACCTCGGGAGAGTATCTCTGGGCTCGAGTACTTGCACGCAAGATC 985
DB	778	GCTGCGCTCTACCTCGGGAGAGTATCTCTGGGCTCGAGTACTTGCACGCAAGATC 837
QY	986	GTCCACAGGGACATCAAGCCATCAACCTGCTCTCTGGGGGATGATGGGCACTGAAGATC 1045
DB	838	GTCCACAGGGACATCAAGCCATCAACCTGCTCTCTGGGGGATGATGGGCACTGAAGATC 897
QY	1046	GCCGACTTTGGCGTCAGCAACAGTTTGAAGGGGACAGCTGCTAGCTGTCCAGCACGGCG 1105
DB	898	GCCGACTTTGGCGTCAGCAACAGTTTGAAGGGGACAGCTGCTAGCTGTCCAGCACGGCG 957
QY	1106	GGAAACCCAGGATTCATGCCCCCGAGGCCATTTCTGATTCGGGCCAGAGCTTCAGTGGG 1165
DB	958	GGAAACCCAGGATTCATGCCCCCGAGGCCATTTCTGATTCGGGCCAGAGCTTCAGTGGG 1017

QY	1166	AAGGCTTGGATGTATGGCCACTGGCGTCACTGTGTAAGTCTTGTCTATGGGAAGTGC 1225
DB	1018	AAGGCTTGGATGTATGGCCACTGGCGTCACTGTGTAAGTCTTGTCTATGGGAAGTGC 1077
QY	1226	CCATTTCATCGAGATTTTCATCTCGCCCTCCACAGGAAGATCAAGAAATGAGCCCGTGTG 1285
DB	1078	CCATTTCATCGAGATTTTCATCTCGCCCTCCACAGGAAGATCAAGAAATGAGCCCGTGTG 1137
QY	1286	TTTCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGAC 1345
DB	1138	TTTCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGAC 1197
QY	1346	AAGATCCCGAGAGAGAGATTTGGGTGCCACACATCAAGTTGCACCTTGGTGGTGCACCAAG 1405
DB	1198	AAGATCCCGAGAGAGAGATTTGGGTGCCACACATCAAGTTGCACCTTGGTGGTGCACCAAG 1257
QY	1406	AACGGGAGGAGCCCTTCCCTTCGGAGGAGGAGCACTGCAGCGTGGTGGAGGTGACAGAG 1465
DB	1258	AACGGGAGGAGCCCTTCCCTTCGGAGGAGGAGCACTGCAGCGTGGTGGAGGTGACAGAG 1317
QY	1466	GGGAGAGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACACAGTGTATCCTGGTGAAG 1525
DB	1318	GAGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACACAGTGTATCCTGGTGAAG 1377
QY	1526	TCCATGCTGAGAAAGCGTTCTTTGGGAAACCGTTTGGAGCCCGCAGGACGGAGGGAAGAG 1585
DB	1378	TCCATGCTGAGAAAGCGTTCTTTGGGAAACCGTTTGGAGCCCGCAGGACGGAGGGAAGAG 1437
QY	1586	CGATCCATGCTGCTCCAGGAAACCTACTGCTGAAAGAGGGTTTGGTGAAGGGGGCAAG 1645
DB	1438	CGATCCATGCTGCTCCAGGAAACCTACTGCTGAAAGAGGGTTTGGTGAAGGGGGCAAG 1497
QY	1646	AGCCAGAGCTCCCGGGCTCCAGGAAGACGAGGCTGCATCCTGA 1690
DB	1498	AGCCAGAGCTCCCGGGCTCCAGGAAGACGAGGCTGCATCCTGA 1542
RESULT 10		
ADB53308		
ID	ADB53308	standard; DNA; 3411 BP.
XX	AC	ADB53308;
XX	XX	
DT	04-DEC-2003	(first entry)
XX		
DE		Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3850.
XX		
KW		toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW		toxicity marker; toxicity progression; drug screening;
KW		primary rat hepatocyte toxicity modelling; gene; ds.
XX		
OS		Rattus norvegicus.
XX		
PN		WO2003065993-A2.
XX		
PD		14-AUG-2003.
XX		
PF		04-FEB-2003; 2003WO-US003482.
XX		
PR		04-FEB-2002; 2002US-0353171P.
PR		13-MAR-2002; 2002US-0363534P.
PR		08-APR-2002; 2002US-0370248P.
PR		10-APR-2002; 2002US-0371134P.
PR		10-APR-2002; 2002US-0371135P.
PR		10-APR-2002; 2002US-0371150P.
PR		11-APR-2002; 2002US-0371413P.
PR		19-APR-2002; 2002US-0373601P.
PR		22-APR-2002; 2002US-0373602P.
PR		22-APR-2002; 2002US-0374139P.
PR		08-MAY-2002; 2002US-0378370P.
PR		09-MAY-2002; 2002US-0378652P.
PR		09-MAY-2002; 2002US-0378653P.

Db 1552 GAAGAAGGATGTGAGAGGGGCAAAAGCCAGAGCTTCCGGAGTCCAGAGATGA 1611
Qy 1678 GGCTGCATCTGAGCCCTGATGACCCAGGGCCACCCCGCAGACACTCATCCCGCGC 1737
Db 1612 GGCTGCATCTGAGTCCCTGATGTCGCCAGGGCCA-TCGGCAGCATGCTCATTCGCTC 1670
Qy 1738 CTCAGAGGCCAC--CCCTCATGCAACAGCGGCCCGCCGAGGCGAGGGGCTGGGGACTG 1795
Db 1671 CTCAGAGGCCACCGCCCTCATGCAATCATGCGCCCTGCAAGGCAGGGGCTGGGGACTG 1730
Qy 1796 CAGCCCACTCC---CGCCCTCCCTCCCTGCTGTCATGACCTCCACGCGACGACGTC 1852
Db 1731 CAGCCCTCTCTGCGCCCTCCCTCACCCTGCTGCTGATGACCTGCGGACAGGATATCC 1790
Qy 1853 AGGACACA-GACTGGAAATGATGTCATTTGGGCTCTTTGGGGCAGGGCT 1899
Db 1791 AGGACAGGATTGGAATGTATCATTTGGGGCTCGGGGCTCCCGGTT 1838

RESULT 11

AZ29223
ID AA229223 standard; cDNA; 2545 BP.

XX AC AA229223;

XX DT 28-FEB-2000 (first entry)

XX DE Human cell signalling protein-2 encoding cDNA.

XX DE Cell signalling protein-2; CSIGP-2; cell proliferation; arteriosclerosis;
KW inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;
KW Addison's disease; multiple sclerosis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 241..1860

FT /*tag= a

FT /product= "Cell Signalling Protein-2"

XX WO9958558-A2.

XX PD 18-NOV-1999.

XX PF 13-MAY-1999; 99WO-US010567.

XX PR 13-MAY-1998; 98US-0085343P.

XX PR 26-AUG-1998; 98US-0098010P.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Bandman O, Hillman JL, Lal P, Yue H, Tang YT, Patterson C;

XX PI Baughn MR, Yang J;

XX DR WPI; 2000-086432/07.

XX DR P-PSDB; AAY44239.

XX PT Human cell signaling proteins useful for, e.g. diagnosing cell
PT proliferative and inflammatory disorders.

XX PS Claim 9; Page 80-81; 90pp; English.

XX CC The present sequence is a cDNA obtained from Incyte clone 640521 of
CC BRSTN03 library. It encodes cell signalling protein-2 (CSIGP-2). It is
CC expressed in reproductive, nervous and developmental tissues. Fragments
CC of CSIGP encoding nucleic acid can be used as hybridisation probe for
CC detecting CSIGP related sequences or allelic variants. Recombinant CSIGP
CC can be produced in host cells by transforming them with genetically
CC engineered vectors. Agonists or antagonists can be used in the treatment
CC of cell proliferative and inflammatory disorders associated with
CC decreased or increased CSIGP expression. CSIGP is used in the diagnosis,
CC prevention and treatment of cell proliferative disorders like

CC arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders
CC like AIDS, Addison's disease, multiple sclerosis, etc

XX SQ Sequence 2545 BP; 542 A; 737 C; 760 G; 506 T; 0 U; 0 Other;

Query Match 30.2%; Score 661; DB 3; Length 2545;

Best Local Similarity 71.0%; Pred. No. 1.1e-133;

Matches 890; Conservative 0; Mismatches 360; Indels 3; Gaps 1;

Qy 439 GCCTTATGCCACGGGGCTGCCAGCCACATCTCCCGGCGCTGGCGGAGCCACCAT 498

Db 618 GCCCTACTACCCCTGAGCTCCCGCAGTCTCGCTCGCTCGCTCGCGCGCGCGACAGT 677

Qy 499 CGAGTCCCACACCTGGCCATCTCAGATGACAGAGTCTGCTGAGCTGAACCGATCAA 558

Db 678 GGAGTCTCACCACTGCTCCATCAGGGTATCAGGACTGTGTGAGCTGAATCAGTATAC 737

Qy 559 GCTGCAGAGTGAAGTTGGCAAGGTCCTACGGTGTGTGAGGCTGCGCTCAACGAAAG 618

Db 738 CCTGAAGGATGAATTGGAAAGGCTCCTATGGTGTCTCAAGTTGGCTTCAATGAAA 797

Qy 619 TGAAGACAGACACTATGCAATGAAGTCTTTTCCAAAAGAGTTACTGAAGCATATGG 678

Db 798 TGACAATACCTACTATGCAATGAAGTCTGTCCAAAAGAGTGTATCCGCGCGCGG 857

Qy 679 CTTTCCAGTCGCTCCCTCCCGAGAGGGTCCCGAGGCTGCCCGAGGAGCACCGCAAGCA 738

Db 858 CTTTCCAGTCGCTCCCTCCCGAGGACCCCGGCGAGTCTCTGGAGGCTGCATCCAGC 917

Qy 739 GCTGTGCTCCCTGGAGCGGTGTACAGGAGATTGCCATCTCTGAAGAGCTGGACACGT 798

Db 918 CAGGGGCCCATTCAGCAGGTGTACACAGGAAATGCCATCTCAAGAGCTGGACACCC 977

Qy 799 GAATGTGTCAAACATGATCGAGTCTCTGGATGACCCAGCTGAGACACCTCTATTGGT 858

Db 978 CAATGTGTGAAGCTGTGGAGTCTCTGGATGACCCCAATGAGGACCATCTGTACATGT 1037

Qy 859 GTTTGACCTCTGAGAAAGGGCGCTCATGAAAGTGCCCTGTGACAAAGCCCTTCTCGGA 918

Db 1038 GTTGAACCTGTCAACGAGGCGCTGATGGAAGTGCCTCCACCTCAACACCTCTCTGA 1097

Qy 919 GGAGCAAGCTCGCTCTACCTCGGGAGCTCATCTGGGCGCTCGAGTACTTGCACTGCCA 978

Db 1098 AGACAGGCGCTTCTACTTCCAGGATCTGATCAAGGGCATCGAGTACTTACACTACA 1157

Qy 979 GAAGATGCTCCAGGGACATCAAGCCATCAACCTGCTCTGGGGAGTATGGCAGT 1038

Db 1158 GAAGATCATCCACCGTGACATCAACCTTCCAACTCTCTGGTGGAGAAATGGGCACT 1217

Qy 1039 GAAGATCGCGACTTTGGCGTCAGCAACACAGTTTGGGGGAAACGACGCTCAGCTGCCAG 1098

Db 1218 CAGATCGCTGACTTTGGTGTGAGCAATGAATTCAGGGCAGTGAAGCTCTCTCTCA 1277

Qy 1099 CACGGCGGAAACCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCGGGCAAGCTT 1158

Db 1278 CACCGTGGGCACGCGCGCTTTCATGGCACCCGAGTCGCTCTCTGAGACCCGCAAGATCTT 1337

Qy 1159 CAGTGGGAAGCGCTTGGATGTATGGGCCACTGCGGCTCAGTGTACTGTCTTGTCTATGG 1218

Db 1338 CTCTGGGAAGCGCTTGGATGTTTGGGCTATGGGTGTGACATATCTCTTGTCTTGG 1397

Qy 1219 GAAGTGCCTATTCAGACGATTTTCATCTCGGCTCCACAGGAAAGATCAAGAATGAGCC 1278

Db 1398 CCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACAGTAAAGATCAAGAGTCAGGC 1457

Qy 1279 CGTGGTGTTCCTGAGGAGCCAGAAATCAGCGAGAGCTCAAGGACCTGATCTCTGAAGAT 1338

Db 1458 CTTGGAATTTCCAGACCCAGCCGACATAGCTGAGGACTTTGAAGGACCTGATCACCGTAT 1517

Qy 1339 GTTAGACAAGAAATCCGAGACGAGAAATTTGGGGTGCAGACATCAAGTTGCACCTTGGT 1398

Db 1518 GCTGGAAGAAGACCCCGAGTCGAGATCGTGTGCGGAATCAAGCTGCACCCCTGGT 1577

Db 1496 CACGAGGATGGGGGAGCGTGGCTCGGAGGATGAGAACTGACGCTGGTGAAGT 1555
QY 1459 GACAGAGGGAGGTTAGAACTGAGTGAAGCTATCCAGCTGAGACAGCGTGAATCT 1518
Db 1556 GACTGAAGAGGAGGTCGAGAACTCAGTCAAAACACATTCAGCTTGGCAACCGTGAATCT 1615
QY 1519 GGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAACCGTTTGGAGCCCGGACGCGAG 1578
Db 1616 GGTGAAGACCAATGATACGTAAACGCTCTTTGGGAACCAATTCGAGGGC--AGCCGGCG 1672
QY 1579 GGAAGAGCGATCCATGCTGCTGCTCAGGAAACCTACTGTTGAAAGAGGTTTGGTGAAGG 1638
Db 1673 GGAGGAACGCTCACTGTCAGCGCTGGAACCTGCTACCAAAACCAACGAGGATG 1732
QY 1639 GGGCAAGAGCCAGAGCTCCCGG 1662
Db 1733 TGAGTCCCTGCTGAGCTCAAGG 1756

RESULT 13

ABK92170

ID ABK92170 standard; DNA; 1804 BP.

XX AC

XX AC

XX DT

XX 15-AUG-2002 (first entry)

XX DE

XX Prostate cancer-associated DNA sequence #56.

XX KW

XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

XX KW

XX gene therapy; gene; ds.

XX OS

XX Mammalia.

XX XX

XX WO200230268-A2.

XX XX

XX 18-APR-2002.

XX XX

XX 12-OCT-2001; 2001WO-US032045.

XX XX

XX 13-OCT-2000; 2000US-00687576.

XX PR

XX 08-DEC-2000; 2000US-00733298.

XX PR

XX 08-DEC-2000; 2000US-00733742.

XX PR

XX 24-JAN-2001; 2001US-0263957P.

XX PR

XX 16-MAR-2001; 2001US-0276791P.

XX PR

XX 16-MAR-2001; 2001US-0276888P.

XX PR

XX 06-APR-2001; 2001US-0281922P.

XX PR

XX 24-APR-2001; 2001US-0286214P.

XX PR

XX 30-APR-2001; 2001US-00847046.

XX PR

XX 04-MAY-2001; 2001US-0288589P.

XX XX

XX (BOSB-) BOS BIOTECHNOLOGY INC.

XX PA

XX XX

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

XX PI

XX WPI; 2002-471335/50.

XX DR

XX P-PSDB; ABG61855.

XX XX

XX Detecting a prostate cancer-associated transcript in a cell in a patient,

XX PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,

XX PT by determining if prostate cancer-associated genes are expressed in a

XX PT prostate tissue.

XX XX

PS Claim 22; Page 342; 436pp; English.

XX PS

XX CC

XX The present invention relates to methods of detecting a prostate cancer-

XX CC associated transcript in a cell from a patient. The method comprises

XX CC contacting a biological sample from the patient with prostate cancer-

XX CC associated polynucleotides (designated PC genes) that selectively

XX CC hybridise to a sequence that is at least 80% identical to them. The

XX CC prostate cancer-associated polynucleotide sequences are differentially

XX CC expressed in prostate tumour tissue or in prostate cancer and are derived

CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences

XX SQ Sequence 1804 BP; 445 A; 519 C; 453 G; 387 T; 0 U; 0 Other;
Query Match 29.7%; Score 651; DB 6; Length 1804;
Best Local Similarity 71.5%; Pred. No. 1.5e-131;
Matches 871; Conservative 0; Mismatches 345; Indels 3; Gaps 1;

QY 439 GCCTTATGCCACGGGGCTGCCAGCCACATCTCCCGGGCGCTGGCGAGGCCACCAT 498
Db 30 GCCCTACTCACCCGTCAGCTCCCGCAGTCTCGCTCGCTGCCCGCGCGCAGT 89
QY 499 CGAGTCCACACACGCTGGCCATCTCAGATGCAGAGACTGCTGCAGCTGAACCATCAA 558
Db 90 GGAGTCTCACACCGTCTCCATCAGGGTATGCAGACTGTGTGAGCTGAATCAGTATAC 149
QY 559 GCTGCAGAGTCAGATTGGCAAGGTCCTACGGTGTGTGAGGCTGGCTTCAACGAAAG 618
Db 150 CTTGAAGATGAATTTGAAAGGGCTCTATGTTGTCTCAAGTTGGCTTAATGAAAA 209
QY 619 TGAAGACAGACACTATGCAATGAAGTCTTTTCCAAAAAGATTTACTGAAGCATGTGG 678
Db 210 TGCAATACCTACTATGCAATGAAGTGTCTTCCAAAAAGAGTGTATCCGCGAGCGG 269
QY 679 GTTTCACGTCGCCCTCCCGAGAGGTCCTCCAGGTCGCCAGGAGGACGAGCAAGCA 738
Db 270 CTTTCCAGTCGCCCTCCCGAGGACCCCGCCAGCTCTCGAGGCTGCATCCAGCC 329
QY 739 GCTGTCGCCCTCGAGGGGTGTACAGAGATTGCCATCTGAAGAGCTGGACCATGT 798
Db 330 CAGGGGCCCATTCAGCAGGTGTACAGGAAATTTGCCATCTCAAGAGCTGGACCATCC 389
QY 799 GAATGTGTCATACTGATTCGAGGTCTCTGGATGACCCAGCTGAGGACACCTCTATTGGT 858
Db 390 CAATGTGTGAAGCTGTGTGGAGTCTCTGGATGACCCCAATGAGGACCATCTGTATGAT 449
QY 859 GTTGTGCTCTCTGAAAGGGGGCCGTCATGGAAGTCCCTGTGACAGCCCTTCTCGGA 918
Db 450 GTTCGAACTGGTCAACCAAGGGCCCGTGTGGAAGTGCCTCCACCTCAAAACCACTCT 509
QY 919 GGAGCAAGCTCGCCTCTACCTGCGGGAGCTCATCTGCGGCTCGAGTACTTGCACCTGCA 978
Db 510 AGACGAGCCCGTCTTCTACTTCCAGGATCTGATCAAGGACATCAGTACTTACACTACCA 569
QY 979 GAAGATCGTCAAGGGACATCAAGGCATCCAACTGCTCTCTGGGGATGATGGGACAT 1038
Db 570 GAAGATCATCCACCGTCGACATCAAACTTCCAACTCTCTGGTGGAGAGATGGGACAT 629
QY 1039 GAAGATCGCGACTTTGCGCTCAGCAACACCTTTTGGGGGACACCGCTCAGCTGCTCAG 1098
Db 630 CAAGATCGCTGACTTTGTGTGACAAATGAATTCAGGGCAGTACCGGCTCTCTCTCTCAA 689
QY 1099 CACGGCGGGAACCCAGCATTTATGCGCCCGGAGGCCATTTCTGATTTCCGCGCAGAGCT 1158
Db 690 CACCGTGGGACGCGCCCTTCAATGGCACCCGAGTCTCTCTGAGACCCGCAAGATCTT 749
QY 1159 CAGTGGGAAGCCCTTGGATGTATGGGCCACTGGGCTCAGTTGCTGCTTTGCTATGG 1218
Db 750 CTCTGGGAAGCCCTTGGATGTTGGGCCATGGGTGTGACACTATCTGCTTTGCTTTGG 809
QY 1219 GAAGTGGCCATTCATCGACCATTTTCATCTGGCCCTCCAGGGAAGATCAAGATGAGCC 1278
Db 810 CCAGTGGCCATTCATGACGAGCGGATCATGTGTTTACAGTAAGATCAAGAGTCAGGC 869
QY 1279 CGTGGTGTTCCTGAGGAGCCAGAAATCAGGAGGAGCTCAAGGACCTGATCTCTGAAGAT 1338

```
Db      870  CCTGGAATTTCCAGACCAGCCGACATAGCTGAGGACTTGAAGGACCTGATCACCCGTAT  929
QY      1339 GTTAGACAGATCCGAGACGAGATTCGGGTGCCAGACATCAAGCTGCACCTTGGGT  1398
Db      930  GCTGGGACAGAACCCCGAGTCGAGGATCGGTGCCGGAATCAAGCTGCACCCCTGGGT  989
QY      1399 GACCAAGAACCGGAGAGCCCTCTCTTCGAGAGGAGCACTGCAGCGTGTGGAGGT  1458
Db      990  CAGGAGCATGGGCGGAGCGGTTCGTCGTCGAGGATGAGAACTGCACGCTGCTCGAAGT  1049
QY      1459 GACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGCAGCACGCTGATCTCT  1518
Db      1050 GACTGAAGAGGAGGTCGAGAACTCAGTCAAAACATTTCCAGCTTGGCAACCGTGATCTCT  1109
QY      1519 GGTGAAGTCCATCTGAGGAGGCTTCTTTCGGAGACCGTTCCTTGGGACCCGTTTGGCCCGAG  1578
Db      1110 GGTGAAGACCATGATACGTAACGCTCTTTCGGGAAACCCCATTCGAGGC---AGCCGGCG  1166
QY      1579 GGAAGAGCGATCCATCTGTCTGCTCCAGGAAACCTACTGTGTAAGAGAGGGTTTGGTGAAGG  1638
Db      1167 GGAGGAACGCTCACTGTCAGCGCTGGAACCTTGCTCACCAAAACCAACAGGGAATG  1226
QY      1639 GGGCAAGAGCCCGAGCTC 1657
Db      1227 TGAGTCCCTGTCTGAGCTC 1245
```

RESULT 14

ID ADB75229 standard; cDNA; 1804 BP.

AC ADB75229;

DI 04-DEC-2003 (first entry)

DE Prostate cancer marker cDNA.

XX Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX Homo sapiens.

XX WO200309814-A2.

XX 06-FEB-2003.

XX 25-JUL-2002; 2002WO-US023913.

XX 25-JUL-2001; 2001US-0307982P.

XX 22-AUG-2001; 2001US-0314356P.

XX 25-SEP-2001; 2001US-0325020P.

XX 12-DEC-2001; 2001US-0341746P.

XX 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JB, Endege WO, Gannavarapu M, Gorbacheva B;

PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;

XX WPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

PT cancer.

XX Disclosure; SEQ ID NO 53; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with

CC the cancerous state of prostate cells. Also disclosed is a method of

CC assessing whether a patient is afflicted with prostate cancer. The method

CC of the invention involves assessing whether a patient is afflicted with

CC prostate cancer by comparing the level of expression of a marker in a

CC patient sample and the normal level of expression of the marker in a

CC control non-prostate cancer sample, where a significant increase in the

CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1804 BP; 445 A; 519 C; 453 G; 387 T; 0 U; 0 Other;

SQ Query Match 29.7%; Score 651; DB 9; Length 1804;

Best Local Similarity 71.5%; Pred. No. 1.5e-131;

Matches 871; Conservative 0; Mismatches 345; Indels 3; Gaps 1;

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GenCore version 5.1.6
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(without alignments)
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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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8	1906.4	87.1	1937	6	AX746188	AX746188 Sequence
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ACCESSION AR221281
VERSION AR221281.1 GI:23328248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2190)
AUTHORS Wei.M.-H., Di Francesco,V. and Beasley,E.M.
TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
JOURNAL Patent: US 6426206-A 1 30-JUL-2002;

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RESULT 2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 Beasley, E.M., Wei, M.H., Bonazzi, V.R., Sanders, R.C. and di
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  Isolated human kinase proteins, nucleic acid molecules encoding
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  Patent: WO 0224920-A. 1. 28-MAR-2002;
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421 TGCACAGCGGCGCTGCCAGCACAATCTCCCGCGGCGCTGGCGAGAGCCACACATCCAGTC 480
QY |||||
505 CCACCACTGCGGCATCTCAGATGCAAGAGACTGCGTGCAGCTGAACCACTACAAGCTGCA 564
Db |||||
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Db |||||
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QY |||||
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Db |||||
841 CTTCTGAGAAAGGGGCCGCTGATGAAGTGCCCTGTGCAAGCCCTTCTCGAGAGAGCA 900
QY |||||
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Db |||||
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Db |||||
1201 CCATTTCTCAGCAGATTCTATCTGCGCCCTCCACAGAGAGATCAAGAAATGAGCCGTGGT 1260
QY |||||
1285 GTTTCCTGAGGAGCGAGAAATCAGCGAGGAGCTCAAGGACCTCATCTGAGAGTGTAGA 1344
Db |||||
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Db |||||
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Db |||||
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2125 GTGGAGAGGGGGTACCTTGGCCACCTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTCA 2184
Db |||||
2101 GTGGAGAGGGGGTACCTTGGCCACCTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTCA 2160
QY |||||
2185 GACGCT 2190
Db |||||
2161 GACGCT 2166

RESULT 4

BC043487

LOCUS

DEFINITION

3575 bp mRNA linear PRI 07-OCT-2003
Homo sapiens calcium/calmodulin-dependent protein kinase kinase 1,
alpha, transcript variant 1, mRNA (cDNA clone MGC:49844
IMAGE:5751570), complete cds.

ACCESSION BC043487

VERSION BC043487.1 GI:27694083

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota;

Mammalia;

Eutheria;

Primates;

Catarrhini;

Hominidae;

Homo.

REFERENCE

AUTHORS

1. (bases 1 to 3575)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.W., Schuler,G.D.,

QY	889	GGAAAGTGCCTGTGACAAAGCCCTTCTCGAGAGCAAGCTGCGCTCTA	948
Db	841	GGAAAGTGCCTGTGACAAAGCCCTTCTCGAGAGCAAGCTGCGCTCTA	900
QY	949	CATCTTGGSCCTCGAGTACTTGCACATGCCAGAGATCGTCCACAGGACATCAAGCCATC	1008
Db	901	CATCTTGGSCCTCGAGTACTTGCACATGCCAGAGATCGTCCACAGGACATCAAGCCATC	960
QY	1009	CAACCTGCTCTTGGGGGATGATGGGCACGTGAAGATCGCGCATTTTGGCGGTGAGCAACCA	1068
Db	961	CAACCTGCTCTTGGGGGATGATGGGCACGTGAAGATCGCGCATTTTGGCGGTGAGCAACCA	1020
QY	1069	GTTTGAGGGGAACGACGCTGACGTGTCAGACGCGCGGAAACCCACGATTCATGCCCCC	1128
Db	1021	GTTTGAGGGGAACGACGCTGACGTGTCAGACGCGCGGAAACCCACGATTCATGCCCCC	1080
QY	1129	CGAGGCCATTTCTGATTCGGCCGACAGCTTCAGTGGGAAGGCTTGGATGATGGCCAC	1188
Db	1081	CGAGGCCATTTCTGATTCGGCCGACAGCTTCAGTGGGAAGGCTTGGATGATGGCCAC	1140
QY	1189	TGGCGTCAAGTTGTACTGCTTTGTCTATGGGAAGTCCCAATTCATCGACGATTTTCATCCT	1248
Db	1141	TGGCGTCAAGTTGTACTGCTTTGTCTATGGGAAGTCCCAATTCATCGACGATTTTCATCCT	1200
QY	1249	GGCCCTCCACAGAGATCAAGAAAGAGCCCGTGTGTTCTGTGAGGAGCCAGAAATCAG	1308
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QY	1429	GGAGAGGAGCACTGACGCGTGTGAGGTGACAGAGGGGAGGTTAAAGATCTCAGTCAG	1488
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QY	1489	GCTCATCCCGACGTGGACCAAGGTGATCTGCTGAGTCCATGCTCAGGAAGGTTCCCTT	1548
Db	1441	GCTCATCCCGACGTGGACCAAGGTGATCTGCTGAGTCCATGCTCAGGAAGGTTCCCTT	1500
QY	1549	TGGGAACCCGTTTGAGCCCCAGGCGACGAGGGAAGAGCGATCCATGCTCTGCTCCAGGAA	1608
Db	1501	TGGGAACCCGTTTGAGCCCCAGGCGACGAGGGAAGAGCGATCCATGCTCTGCTCCAGGAA	1560
QY	1609	CCTACTGTGAAAGAGGTTTGGTGAAGGGGCAAGAGCCAGAGCTCCCCGGCGTCCA	1668
Db	1561	CCTACTGTGAAAGAGGTTTGGTGAAGGGGCAAGAGCCAGAGCTCCCCGGCGTCCA	1620
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Db	1621	GGAAGACGAGGCTGCATCTGAGCCCTGATGACCCAGGCGCCACCCGCGAGGAGCACTC	1680
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QY	1909	CCATCTCTCTTCTTGGCCCTTCTGGGCTGACCCCATCTGCTGGGGAAACCGGGTGCCC	1968
Db	1861	CCATCTCTCTTCTTGGCCCTTCTGGGCTGACCCCATCTGCTGGGGAAACCGGGTGCCC	1920

QY	1969	ATGAGGCTCAGAAATGCAACCCGCTGTTGGCATGGCTGGGGCAGAGGCAGAGGCA	2028
Db	1921	ATGAGGCTCAGAAATGCAACCCGCTGTTGGCATGGCTGGGGCAGAGGCAGAGGCA	1980
QY	2029	GGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACCAACGGAAGAGACTCCCGCTGGG	2088
Db	1981	GGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACCAACGGAAGAGACTCCCGCTGGG	2040
QY	2089	GCCGGGCGAGCCTGGCTCAGCTGCCACAGGCATATGTTGGAGAGGGGGGTACCTGCCCA	2148
Db	2041	GCCGGGCGAGCCTGGCTCAGCTGCCACAGGCATATGTTGGAGAGGGGGGTACCTGCCCA	2100
QY	2149	CCTTGGGGTGGGCACACAGACTCTTGTCTATTAGACGCT	2190
Db	2101	CCTTGGGGTGGGCACACAGACTCTTGTCTATTAGACGCT	2142
RESULT 5			
AF425232			
LOCUS			
DEFINITION	Homo sapiens CamKK alpha protein mRNA, complete cds.	3536 bp	mRNA linear PRI 04-OCT-2002
ACCESSION	AF425232		
VERSION	AF425232.1	GI:23499313	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
1	(bases 1 to 3536)		
AUTHORS	Tascadda, F., Carra, S., Harvey, M. and Barden, N.		
TITLE	Characterization of human CamKK alpha gene structure		
JOURNAL	Unpublished		
REFERENCE			
2	(bases 1 to 3536)		
AUTHORS	Tascadda, F., Carra, S., Harvey, M. and Barden, N.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-SEP-2001) Pharmacology, University of Modena and Reggio Emilia, Campi 183, Modena, MO 41100, Italy		
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ORIGIN			
Query Match	96.5%	Score 2114.2	DB 9; Length 3536;
Best Local Similarity	99.9%	Pred. No. 0;	
Matches 2116;	Conservative	0; Mismatches	3; Indels 0; Gaps 0;
QY	72	GCAGCAGGAGCAGTGGGGCCGCCCGCGGCGCACGACACTGTCCCGCGGCCAGGT	131
Db	1	GCAGCAGGAGCAGTGGGGCCGCCCGCGGCGCACACTGTCCCGCGGCCAGGT	60
QY	132	TCCCAACAGGCTACGACAGAGAACCCCTTGTACTGAAGCATGGAGGGGTCCAGCTG	191
Db	61	TCCCAACAGGCTACGACAGAGAACCCCTTGTACTGAAGCATGGAGGGGTCCAGCTG	120

Qy 192 TCTGCTGGCAGGATCCTCGGCAGAGCTGGTAGAACGGGTGGCAGGCATCGATGTGACTC 251
Db 121 TCTGCTGCCAGGATCCTCGGCAGAGCTGGTAGAACGGGTGGCAGGCATCGATGTGACTC 180
Qy 252 ACTTGGAGGAGCAGATGGTGGCCAGAGCCCTACTAGAAACGGTGTGGACCCCCACACAC 311
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Qy 312 GGGCCAGAGCTGCTGTGTGATCCTCGCAGTACTTCAAGACTCTCTCCAGCCCGGCTA 371
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Db 721 ACCACGTGAATGTGGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGAGGACAACTCT 780
Qy 852 ATTTGGTGTGACCTCTCAGAAAGGGGCCCGCTCATGGAAGTGCCTGTGACAAAGCCCT 911
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Qy 2172 TCTTGTCTATTTCAGACGCT 2190
Db 2101 TCTTGTCTATTTCAGACGCT 2119

RESULT 6

AF425301

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

AF425301 3529 bp mRNA linear PRI 04-OCT-2002
Homo sapiens CAMKK alpha protein (CAMKK1) mRNA, complete cds.

AF425301

AF425301.1 GI:23499315

Homo sapiens (human)

ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 3529)	
TITLE	Harvey.M., Carra.S., Tascadda.F. and Barden.N.	
JOURNAL	Characterization of human CAMKK alpha gene structure	
REFERENCE	Unpublished	
AUTHORS	2 (bases 1 to 3529)	
TITLE	Harvey.M., Carra.S., Tascadda.F. and Barden.N.	
JOURNAL	Direct Submission	
FEATURES	Submitted (27-SEP-2001) Neuroscience, CHUL, 2705 Blvd. Laurier, Ste-Foy, Quebec G1V4G2, Canada	
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QY	130 GTTCCCAACAGGCTACGAGAGAACCCCTTGACTGAAGCAATGGAGGGGGTCCAGC	189
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LOCUS Sequence 14 from Patent WO0146397.
DEFINITION AX179641
ACCESSION AX179641
VERSION AX179641.1 GI:15132054
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Yang, J., Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Reddy, R.,
Yue, H., Yao, M.G., Lal, P. and Khan, F.A.
TITLE Human kinases
JOURNAL Patent: WO 0146397-A 14 28-JUN-2001;
Incyte Genomics, Inc. (US)
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LOCUS AX746188 1937 bp DNA linear PAT 13-JUN-2003
DEFINITION Sequence 39 from Patent WO0208399.
ACCESSION AX746188
VERSION AX746188.1 GI:31746174
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
AUTHORS Yue, H., Khan, F.A., Gururajan, R., Hafalia, A.J., Chawla, N.K., Arvizu, C.S., Ramkumar, J., Gandhi, A.R., Policky, J.L., Baughn, M.R., Tribouley, C.M., Bandman, O., Nguyen, D.B., Lu, Y., Burford, N., Lal, P., Ding, L., Yao, M.G., Elliott, V.S., Recipon, S.A., Kearney, L., Lu, D.A., Greenwald, S.R., Tang, Y.T., Xu, Y., Walsh, R.T., Gietzen, K.J., Yang, J., Jackson, J.L. and Thornton, M.
TITLE Human kinases
JOURNAL Patent: WO 0208399-A 39 31-JAN-2002;
FEATURES Incyte Genomics, Inc. (US) ; Thornton, Michael (US)
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Best Local Similarity 99.7%; Pred. No. 0;
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LOCUS
DEFINITION Sequence 7 from Patent WO0220800.
ACCESSION AX455761
VERSION AX455761.1 GI:21714788
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Meyers,R.A. and Silos-Santiago,I.
TITLE 16658, 14223, and 16002, novel human kinases and uses therefor
JOURNAL Patent: WO 0220800-A 7 14-MAR-2002;
MILLENNIUM PHARM INC (US)

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Best Local Similarity 98.9%; Pred No. 1.1e-312;
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DEFINITION Sequence 9 from Patent WO0220800.
ACCESSION AX455763
VERSION AX455763.1 GI:21714790
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ORGANISM Homo sapiens
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REFERENCE 1
AUTHORS Meyers, R.A. and Silos-Santiago, I.
TITLE 1658, 14223, and 16002, novel human kinases and uses therefor
JOURNAL Patent: WO 0220800-A 9 14-MAR-2002;
MILLENNIUM PHARM INC (US)
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VERSION AX1166519.1 GI:14546864
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
1. Flanagan, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
Flanagan, P. and Clary, D.S.
Novel human protein kinases and protein kinase-like enzymes
Patent: WO 0138503-A 10 31-MAY-2001;
Sugen, Inc. (US)
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Matches 1513; Conservative 0; Mismatches 2; Indels 30; Gaps 2;

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ACCESSION  BC031647
VERSION    BC031647.1  GI:21594835
KEYWORDS  MGC.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257

2 (bases 1 to 2469)

12477932

Strausberg, R.

Direct Submission

Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseg, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

USA

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27437010.

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ORIGIN

Query Match 64.0%; Score 1401.6; DB 9; Length 2469;
Best Local Similarity 92.3%; Pred. No. 2.1e-266;
Matches 1534; Conservative 0; Mismatches 14; Indels 114; Gaps 1;

Qy	91	CGCCCGCGGGCCACGACACTGTCGCCGGGCCCGCCAGGTTCCCAACAAGGCTACGAG	150
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Qy	151	AAGAACCCCTTGACTAAGCAATGAGAGGGGGTCCAGCTGTCTGCTGCCAGATCTCG	210
Db	61	AAGAACCCCTTGACTAAGCAATGAGAGGGGGTCCAGCTGTCTGCTGCCAGATCTCG	120
Qy	211	GGCAGAGCTGTAGAAACGGGTGGCAGCCATCGATGTGACTCACCTTGAGGAGGAGGATGG	270
Db	121	GGCAGAGCTGTAGAAACGGGTGGCAGCCATCGATGTGACTCACCTTGAGGAGGAGGATGG	180
Qy	271	TGGCCCGAGAGCTACTAGAAACCGTGTGGACCCCGCCACCGGCGCAGAGTGCCTCTGT	330
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Qy	331	GATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCGCTAGCTCTCAGCCAGGAAGCT	390
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Qy	391	TTCCCTACAGAGCGGCGCAGCAGAAAGCTATCTGGAGCGCAGGCTGGGCCCTTATGCCAC	450
Db	301	TTCCCTACAGAGCGGCGCAGCAGAAAGCTATCTGGAGCGCAGGCTGGGCCCTTATGCCAC	360
Qy	451	GGGCGCTGCGACCAATCTCCCGCGGCGCTGGCGGAGGCCACCATCGAGTCCACCA	510
Db	361	GGGCGCTGCGACCAATCTCCCGCGGCGCTGGCGGAGGCCACCATCGAGTCCACCA	420
Qy	511	CGTGGCCATCTCAGATCAGAGGACTGCGTGACGTGAACAGTACAGCTGCGAGAGTGA	570
Db	421	CGTGGCCATCTCAGATCAGAGGACTGCGTGACGTGAACAGTACAGCTGCGAGAGTGA	480
Qy	571	GATTGGCAAGGGTGCCTTACGCTGTGGTGAAGCTGGCGCTTACAAAGTGAAGACAGACA	630
Db	481	GATTGGCAAGGGTGCCTTACGCTGTGGTGAAGCTGGCGCTTACAAAGTGAAGACAGACA	540
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Qy	691	CCCTCCCGCAGAGGGTCCAGGCTGCCAGGAGGACCCAGCAGCTGCTGCCCT	750
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Qy	751	GGAGCGGGTGTACAGGAGATGTCATCTCTGAAGAAGCTGACCAACGTAATGTGGTCAA	810
Db	661	GGAGCGGGTGTACAGGAGATGTCATCTCTGAAGAAGCTGACCAACGTAATGTGGTCAA	720
Qy	811	ACTGATCGAGTCTCTGATGACCCAGCTGAGGACCACTCTATTG	856
Db	721	ACTGATCGAGTCTCTGATGACCCAGCTGAGGACCACTCTATTG	780

Qy	857	-----	856
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Db	841	TGAGCAGCAAGACAGTGCATCCAGTGGGCTGCGCGCTCAGTGTTCACCTCTCTGAGAAA	900
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Qy	937	CCTGCGGGAGCTCATCTGCGGCTCGAGTACTGCACTGCCAGAGATCGTCCACACGGA	996
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Qy	1057	CGTCAGCAACAGTTCGAGGGGAACGACGCTCAGCTGTCCAGCAGCGGGGAACCCGAC	1116
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Qy	1117	ATTTCATGCGCCCGGAGGCCATTTCTGATTCGCGCCAGAGCTTCAGTGGGAAGGCTTTGGA	1176
Db	1141	ATTTCATGCGCCCGGAGGCCATTTCTGATTCGCGCCAGAGCTTCAGTGGGAAGGCTTTGGA	1200
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Qy	1357	GACGAGAAATTGGGTGTCAGACATCAAGTTGACACCTTTGGGTGACCAAGAAACGGGGAGGA	1416
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Qy	1417	GCCCTTTCCTTCGAGAGGAGGACCTCGAGGTGTTGAGGTGACAGAGGGGAGGTAA	1476
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Qy	1537	GAGCGTTCCTTTGGGAAACCGTTTGGAGCCCGAGGACCGAGGGAAGAGCGATCCATGTC	1596
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RESULT 13

LOCUS BC017529
DEFINITION Mus musculus calcium/calmodulin-dependent protein kinase 1,
alpha, mRNA (cDNA clone MGC:27706 IMAGE:4924656), complete cds.
ACCESSION BC017529
VERSION BC017529.1
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Db	722	AGATTGCCATTCAAAGAGCTGGACAACGTGAATGTAGTCAAAATTGATCGAGGTCTCTGG	751
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Db	782	ATGATCCCGTGAAGACAACCTCTATTTTGGTGTGACCTCTTGAGAAAGGGCCAGTCA	841
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Db	842	TGGAAGTGCCCTGTGACAAGCCCTTCCAGAGAGCAAGCTCGCTCTACTTCGGGGACA	901
Qy	948	TCATCTGGGCCTCGAGTACTTGCACATGCCAGAAAGATCGTCCACAGGGACATCAAGCCAT	1007
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Qy	1008	CCAACTGCTCTCGGGGGATGATGGGCACTGAAGATCGCCGACTTTGGCGGTGAGCAACC	1067
Db	962	CTAACCTACTCTTTGGGGAGCGACGGGCAATGTGAAGATCGCCGACTTTTGGTGTGAGTAACC	1021
Qy	1068	AGTTTGAGGGGAACGACGCTGACGTGTCCACGACGGCGGGAACCCACAGCAATTCATGGCCC	1127
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Qy	1128	CCGAGGCCATTTCGTATCCGGCCAGAGCTTCAGTGGGAAGGCTTGGATGTATGGGCCA	1187
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Qy	1188	CTGGCTGCAAGTTGTACTCTTTGTCTATGGGAAGTGCCTCATTCATCGAGATTTCAATCC	1247
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Qy	1368	GGGTGCCAGACATCAAGTGTGACCCCTTTGGGTGACCAAGAAACGGGAGGAGCCCTTCCTT	1427
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Qy	1428	CGGAGGAGGACACTGCAGCGTGTGTGAGGTGACAGAGGGGGAGGTTAAGATCTAGTCA	1487
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Qy	1488	GGCTCATCCCGAGCTGCAGCACCGTGTACTGTGTGAAGTCCATGCTCAGAGAGGTTCCCT	1547
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Qy	1668	AGGAAGACGAGGCTGCATCTTCGAGCCCTGTCATCACCCAGGGGCCACCCCGGACACACT	1727
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Qy	1843	ACGCACTGCCAGGACAC-GACTGGAATGTATGTCTATTTGGGGTCTTGGGGGCAAGGGTCC	1901
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Qy 1902 CACAGGCCATCTCTCTCTCTG 1925
Db 1861 TCCTCTCTGTCTGAATCATCTTG 1884

RESULT 14
S83194
LOCUS S83194 3429 bp mRNA linear ROD 11-FEB-1997
DEFINITION Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats,
          brain, mRNA, 3429 nt].
ACCESSION S83194
VERSION S83194.1 GI:1936160
KEYWORDS
SOURCE
ORGANISM Rattus sp.
          Rattus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 3429)
          Okuno,S., Kitani,I. and Fujisawa,H.
          Evidence for the existence of Ca2+/calmodulin-dependent protein
          kinase IV kinase isoforms in rat brain
          J. Biochem. 119 (6), 1176-1181 (1996)
JOURNAL 96425004
MEDLINE 8927455
PUBMED
REMARK
          GenBank staff at the National Library of Medicine created this
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          This sequence comes from Fig. 1.
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Qy	118	CCCGGGCGCCGAGGTTCCCAACAAGGCTACGCAAGAACCCTTGACTGAAGCAATGGA	177		
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Qy	178	GGGGGGTCCAGCTCTCTGTGCTCCAGGATCTTCGGGCGAGACTGGTAGAAACGGGTGGCAGC	237		
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QY	238	CATCGATGTGACTCACTTTGGAGGAGGACAGATGGTGGCCACGAGGCTTACTAGAAAACGGTGT	297
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DB	292		
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QY	478	GGCCTGGCGGAGGCCACCATCTGAGTCCCACCACTGGGCCATCTCAGATGCAGAGGACTG	537
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DB	892	CCTCGAGTACTTGCATGCCAGAAAGATTGTGCAAGGGACATCAAGCCGCTCCAATCTGCT	951
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QY	1318	CAAGGACCTGATCTCTGAAGATGTTAGACAAGAATCCGACGACGAGAAATTCGGGGTCCAGA	1317
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DEFINITION	Rattus norvegicus mRNA for Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase alpha, complete cds.		
ACCESSION	AB023658		
VERSION	AB023658.1	GI:4512333	
KEYWORDS	Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
AUTHORS	1 (sites)		
TITLE	Okuno,S., Kitani,T. and Fujisawa,H.		
	Evidence for the existence of Ca2+/calmodulin-dependent protein kinase IV kinase isoforms in rat brain		
JOURNAL	J. Biochem. 119 (6), 1176-1181 (1996)		
MEDLINE	96425004		
PUBMED	8827455		
REFERENCE	2 (bases 1 to 3411)		
AUTHORS	Fujisawa,H. and Okuno,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-FEB-1999) Hitoshi Fujisawa, Asahikawa Medical College, Department of Biochemistry; Nishikagura 4-5-3-11, Asahikawa 078-8510, Japan [E-mail:okuno@asahikawa-med.ac.jp, Tel:+81-166-68-2340, Fax:+81-166-68-2349]		
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 04:12:53 ; Search time 87 Seconds
(without alignments)
1831.456 Million cell updates/sec

Title: US-10-690-617-2

Perfect score: 2634

Sequence: 1 MEGGPAVCCQDPRAELVERV.....FEGGKSPCLPGVQDEAAS 505

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2470	93.8	520	4 Q8N5S9	Q8n5s9 homo sapien
3	2468	93.7	505	11 P97756	P97756 rattus norv
4	2461	93.4	505	11 Q8VBV2	Q8vby2 mus musculu
5	2452	93.1	505	11 Q84572	Q84572 rattus norv
6	2419	91.8	505	11 Q9R054	Q9r054 mus musculu
7	1834	69.6	523	13 Q8AYR1	Q8ayr1 xenopus lae
8	1537.5	58.4	541	4 Q8WV04	Q8wy04 homo sapien
9	1536	58.3	541	4 Q81UG3	Q81ug3 homo sapien
10	1525.5	57.9	557	4 Q94883	Q94883 homo sapien
11	1525	57.9	541	11 Q9QZT7	Q9qzt7 mus musculu
12	1518.5	57.6	533	4 Q96RR3	Q96rr3 homo sapien
13	1518.5	57.6	588	4 Q96RR4	Q96rr4 homo sapien
14	1517	57.6	533	4 Q96RP2	Q96rp2 homo sapien
15	1517	57.6	588	4 Q96RP1	Q96rp1 homo sapien
16	1498	56.9	588	4 Q9Y5N2	Q9y5n2 homo sapien

17	1495	56.8	588	11 Q8C078	Q8c078 mus musculu
18	1494	56.7	587	11 Q88831	Q88831 rattus norv
19	1488	56.5	588	11 Q8CH42	Q8ch42 mus musculu
20	1472.5	55.9	417	4 Q9UER3	Q9uer3 homo sapien
21	1422	54.0	579	11 Q8C0C3	Q8c0c3 mus musculu
22	1358.5	51.6	503	11 Q8BXM8	Q8bxm8 mus musculu
23	1342	50.9	498	4 Q8WY03	Q8wy03 homo sapien
24	1340.5	50.9	498	4 Q8IUG2	Q8iug2 homo sapien
25	1323	50.2	545	4 Q8WY05	Q8wy05 homo sapien
26	1321.5	50.2	490	4 Q8WY06	Q8wy06 homo sapien
27	1197.5	45.5	419	11 Q80TS0	Q80ts0 mus musculu
28	1047	39.7	432	5 Q8T8D4	Q8t8d4 caenorhabdi
29	1037	39.4	365	4 Q8N3I4	Q8n3i4 homo sapien
30	949	36.0	269	4 Q9BWE9	Q9bwe9 homo sapien
31	629.5	23.9	180	4 Q9UES2	Q9ues2 homo sapien
32	557	21.1	518	3 Q9Y898	Q9y898 emericella
33	527.5	20.0	420	10 Q9AUR9	Q9aur9 oryza sativ
34	526.5	20.0	396	10 Q93V58	Q93v58 arabidopsis
35	520.5	19.8	407	10 Q8LP06	Q8lp06 arabidopsis
36	512	19.4	382	10 Q9M1T5	Q9m1t5 arabidopsis
37	503	19.1	402	10 Q9FKJ2	Q9fkj2 arabidopsis
38	478.5	18.2	217	3 Q9UTZ4	Q9utz4 schizosacch
39	468	17.8	1246	3 Q9P3E9	Q9p3e9 neurospora
40	448	17.0	440	10 Q24343	Q24343 sorghum bic
41	446.5	17.0	452	10 Q84VQ3	Q84vq3 arabidopsis
42	437	16.6	440	10 Q24342	Q24342 sorghum bic
43	436.5	16.6	511	10 Q40544	Q40544 nicotiana t
44	434	16.5	461	10 Q82051	Q82051 sorghum bic
45	431.5	16.4	514	10 Q9M726	Q9m726 lycopersico

ALIGNMENTS

RESULT 1

ID	Q8BQH3	PRELIMINARY;	PRT;	505 AA.
AC	Q8BQH3;			
DT	01-JUN-2001 (TREMREL. 17, Created)			
DT	01-JUN-2001 (TREMREL. 17, Last sequence update)			
DT	01-OCT-2003 (TREMREL. 25, Last annotation update)			
DE	Hypothetical protein (CamKK alpha protein)			
DE	(Calcium/calmodulin-dependent protein kinase 1 alpha, isoform a).			
DE	a).			
GN	DKFZP761M0423 OR CAMKK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Amygdala;			
RX	MEDLINE=21154917; PubMed=11230166;			
RA	Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,			
RA	Ansorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,			
RA	Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,			
RA	Mewes H.W., Othenwaelder B., Obermaier B., Tampe J., Heubner D.,			
RA	Wambutt R., Korn B., Klein M., Poustka A.;			
RA	"Towards a Catalog of Human Genes and Proteins: Sequencing and			
RT	Analysis of 500 Novel Complete Protein Coding Human cDNAs.";			
RL	Genome Res. 11:422-435 (2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Tascadda F., Carra S., Harvey M., Barden N.;			
RT	"Characterization of human CamKK alpha gene structure.";			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	MEDLINE=22368257; PubMed=12477932;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AL36576; CAB66511.1; -;
 DR EMBL; AF425232; AN37386.1; -;
 DR EMBL; AF425301; AN37387.1; -;
 DR EMBL; BC043487; AAH43487.1; -;
 DR HSSP; Q63450; 1A06.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW Hypothetical protein; ATP-binding; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 505 AA; 55735 MW; 92A055D20E487C86 CRC64;
 Query Match 99.7%; Score 2626; DB 4; Length 505;
 Best Local Similarity 99.8%; Pred. No. 3e-204;
 Matches 504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MEGGPVCCODPRAELVERVAADVTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
 DB 1 MEGGPVCCODPRAELVERVAADVTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
 QY 61 LLPARPSLSARKLSLQERPAGSYLEAAGPYATGTPASHISPRAWRRTTIESHVAISDAE 120
 DB 61 LLPARPSLSARKLSLQERPAGSYLEAAGPYATGTPASHISPRAWRRTTIESHVAISDAE 120
 QY 121 DCVOLNOYKLOQSEIGKAGYGVRLAYNESDRHYAMKVLKKLLKQYGFPRPPRGSG 180
 DB 121 DCVOLNOYKLOQSEIGKAGYGVRLAYNESDRHYAMKVLKKLLKQYGFPRPPRGSG 180
 QY 181 AAGGPAKQLPLERVYQETAILKLDHNVVKLIEVLDDPAEDNLYLFDLLRKGPMVE 240
 DB 181 AAGGPAKQLPLERVYQETAILKLDHNVVKLIEVLDDPAEDNLYLFDLLRKGPMVE 240
 QY 241 VPCDKPSEARLYLRDVLIGLEYLHCQKIVHRDIKPSNLLGDDGHVXIADFGVSNQF 300
 DB 241 VPCDKPSEARLYLRDVLIGLEYLHCQKIVHRDIKPSNLLGDDGHVXIADFGVSNQF 300
 QY 301 EGNDALQSSTAGTAPAFMAPEAISDSGSGSKALDVWATGVTLYCFYVYKCPFIIDFILA 360
 DB 301 EGNDALQSSTAGTAPAFMAPEAISDSGSGSKALDVWATGVTLYCFYVYKCPFIIDFILA 360

QY 361 LHRKIKNEPVVPEEPISEELKDLILKMLDKNPETRIGVDPDKLHPWVTKNGEPLPSE 420
 DB 361 LHRKIKNEPVVPEEPISEELKDLILKMLDKNPETRIGVDPDKLHPWVTKNGEPLPSE 420
 QY 421 EEHCVVVEVEGEVKNVRLIPSWTIVLVKMLRKRSFGNPFEPQARRERSMSAPGNL 480
 DB 421 EEHCVVVEVEGEVKNVRLIPSWTIVLVKMLRKRSFGNPFEPQARRERSMSAPGNL 480
 QY 481 LVKEGFGEGCKSPFLPGVQDEAAS 505
 DB 481 LVKEGFGEGCKSPFLPGVQDEAAS 505
 RESULT 2
 Q8N5S9 PRELIMINARY; PRT; 520 AA.
 AC Q8N5S9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to hypothetical protein DKFp761M0423.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC031647; AAH31647.1; -;
 DR Genew; HGNC:1469; CAMKK1.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 520 AA; 57451 MW; 44B21EC1F25420F4 CRC64;
 Query Match 93.8%; Score 2470; DB 4; Length 520;
 Best Local Similarity 92.3%; Pred. No. 1.4e-191;
 Matches 480; Conservative 0; Mismatches 2; Indels 38; Gaps 1;
 QY 1 MEGGPVCCODPRAELVERVAADVTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
 DB 1 MEGGPVCCODPRAELVERVAADVTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
 QY 61 LLPARPSLSARKLSLQERPAGSYLEAAGPYATGTPASHISPRAWRRTTIESHVAISDAE 120
 DB 61 LLPARPSLSARKLSLQERPAGSYLEAAGPYATGTPASHISPRAWRRTTIESHVAISDAE 120
 QY 121 DCVOLNOYKLOQSEIGKAGYGVRLAYNESDRHYAMKVLKKLLKQYGFPRPPRGSG 180
 DB 121 DCVOLNOYKLOQSEIGKAGYGVRLAYNESDRHYAMKVLKKLLKQYGFPRPPRGSG 180
 QY 181 AAGGPAKQLPLERVYQETAILKLDHNVVKLIEVLDDPAEDNLYLFDLLRKGPMVE 228
 DB 181 AAGGPAKQLPLERVYQETAILKLDHNVVKLIEVLDDPAEDNLYLFDLLRKGPMVE 240
 QY 229 -----VFLLRKGPMVEVPCDKPFSEARLYLRDVLIG 262

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Db 241 STNIAKPSHLLPSBQQSGSQTAAKRSVDFLLKRGVMEVPCDKPSEQARLYLRDVLIG 300
Qy 263 LEYLHCQKIVHRDIKPSNLLGDDGHVXIADFGVSNQFEGNDAQLSSTAGTAPAFMAPEAI 322
Db 301 LEYLHCQKIVHRDIKPSNLLGDDGHVXIADFGVSNQFEGNDAQLSSTAGTAPAFMAPEAI 360
Qy 323 SDSGQSPGSKALDVWATGVTLYCFYVKGCPFDIDFILALHKKIKNEPVPVPEEPISEEL 382
Db 361 SDSGQSPGSKALDVWATGVTLYCFYVKGCPFDIDFILALHKKIKNEPVPVPEEPISEEL 420
Qy 383 KDLILKMLDKNPETRIGVDPDKLHPWVTKNGEELPSEEEHCSVVVTEGEVKNSVRLIP 442
Db 421 KDLILKMLDKNPETRIGVDPDKLHPWVTKNGEELPSEEEHCSVVVTEGEVKNSVRLIP 480
Qy 443 SWTTVILVKMLRKRSFGNPFEPQARRERSMSAPGNLLV 482
Db 481 SWTTVILVKMLRKRSFGNPFEPQARRERSMSAPGNLLV 520

RESULT 3
P97756
ID P97756 PRELIMINARY; PRT; 505 AA.
AC P97756;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CA2+/calmodulin-dependent protein kinase IV kinase isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96425004; PubMed=8827455;
RA Okuno S., Kitani T., Fujisawa H.;
RT "Evidence for the existence of Ca2+/calmodulin-dependent protein
RT kinase IV kinase isoforms in rat brain.";
RL J. Biochem. 119:1176-1181(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Fujisawa H., Okuno S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; S83194; AAB46910.1; -.
DR EMBL; AB023658; BAA75246.1; -.
DR HSP; Q63450; IAO6
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD00001; Prot kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 505 AA; 55907 MW; 6B268780AC9B67E1 CRC64;

Query Match 93.7%; Score 2468; DB 11; Length 505;
Best Local Similarity 93.5%; Pred. No. 1.9e-191;
Matches 472; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MEGGPAVCCQDPRAELVERVAIDVTHLEEDGPEPTNGVDPPPPARAASVIGPSTSR 60
Db 1 MERSFAVCCQDPRAELVERVAISVAHLEAEAGEPEPASNGVDPPPPARAASVIGSASR 60
Qy 61 LLPAPRPSLSARKLSQERPAGSLEAQAGFYATGPASHISPRAMRRPTIESHHVAISDAE 120
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Db 61 PTPVRPSLSARKLSQERPAGSLEAQAGFYATGPASHISPRAMRRPTIESHHVAISDAE 120
Qy 121 DCVOLNQYKLOSEICKGAYGVVRLAYNESEDRHYAMKVLSSKKLLKQYGFRRPPRRGSQ 180
Db 121 DCVOLNQYKLOSEICKGAYGVVRLAYNEREDRHYAMKVLSSKKLLKQYGFRRPPRRGSQ 180
Qy 181 AAGGPAKQLPLSERVQETAILKKLDHVVNVKUIEVLDDPAEDNLYLVFLLRRKGPVME 240
Db 181 APOGPAKQLPLSERVQETAILKKLDHVVNVKUIEVLDDPAEDNLYLVFLLRRKGPVME 240
Qy 241 VPCDKPSEEEARLYLRDVLILGLVLCQKIVHRDIKPSNLLGDDGHVXIADFGVSNQF 300
Db 241 VPCDKPPEEQARLYLRDVLILGLVLCQKIVHRDIKPSNLLGDDGHVXIADFGVSNQF 300
Qy 301 EGNDALQSSTAGTAPAFMAPEAISDSGQSPGSKALDVWATGVTLYCFYVKGCPFDIDFLIA 360
Db 301 EGNDALQSSTAGTAPAFMAPEAISDTGQSPGSKALDVWATGVTLYCFYVKGCPFDIDEYILA 360
Qy 361 LHRKIKNEPVPVPEEPISEELKDLILKMLDKNPETRIGVDPDKLHPWVTKNGEELPSE 420
Db 361 LHRKIKNEAVVPPEPEVSEELKDLILKMLDKNPETRIGVSDIKLHPWVTKHGEPLPSE 420
Qy 421 EEHCSVVTEGEVKNSVRLIPSWTTVILVKMLRKRSFGNPFEPQARRERSMSAPGNL 480
Db 421 EEHCSVVETEEVKNSVKLIPSWTTVILVKMLRKRSFGNPFEPQARRERSMSAPGNL 480
Qy 481 LVKSGFGGKSPBLPGVQDEAAS 505
Db 481 LLKSGGEGKSPBLPGVQDEAAS 505

RESULT 4
Q8VBY2
ID Q8VBY2 PRELIMINARY; PRT; 505 AA.
AC Q8VBY2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase alpha (Similar to
DE calcium/calmodulin-dependent protein kinase kinase 1, alpha).
GN CAMKK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Blaesser F., Ho N., Chatila T.A.;
RT "Genomic Organization of Murine CamKKalpha Gene.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF461706; AAL67849.1; -.
DR EMBL; AF461702; AAL67849.1; JOINED.
DR EMBL; AF461703; AAL67849.1; JOINED.
DR EMBL; AF461704; AAL67849.1; JOINED.
DR EMBL; AF461705; AAL67849.1; JOINED.
DR EMBL; BC017529; AAL17529.1; -.
DR MGD; MGI:1891766; Camkk1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
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Db 486 RRERSMSAPGNLLIKQVSEVAKSDLPDVEDEGTS 523
RESULT 8
Q8WY04 PRELIMINARY; PRT; 541 AA.
AC Q8WY04;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CAMKK beta 1 isoform (Similar to calcium/calmodulin-dependent protein
DE kinase kinase 2, beta).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF321387; AAL37217.1; -.
DR EMBL; BC026060; AAH26060.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 541 AA; 59587 MW; 3D3AC0943A7D7941 CRC64;

Query Match 58.4%; Score 1537.5; DB 4; Length 541;
Best Local Similarity 62.0%; Pred. No. 6.1e-116;
Matches 300; Conservative 79; Mismatches 74; Indels 31; Gaps 5;

QY 30 EADGPEPTRNGVDPPPRARAASVPGSTSRLLPARPSLSARKLSLQER-----PAGSYL 84
Db 75 EADGQEVF-----LDSSGSQ---ARPHLSGRKLSLQERSQGLAGGSL 115

QY 85 EAQAG-----PYATGPASHISPRAWRPPTIESHHVAISDAEDCVQLNKLQSEIGKGA 138
Db 116 DMNGRCICPLSPYSPVSSPSSPSSPSSPSSPSSPSSPSSPSSPSSPSSPSSPSSPSSPSS 175

QY 139 YGVVRLAYNESEDRHYAMKVLKSKLLKQYGFRRPRPRPGSQAAQGPAPKQLPLSERVYQ 198
Db 176 YGVVKKLAYNENDNTYYAMKVLKSKLLKQYGFRRPRPRPGSQAAQGPAPKQLPLSERVYQ 235

QY 199 ETAILKKLDHNVVVKLTVELDDPAEDNLVLFVLLRKGPMVEVPCDKPFEEQARLYLRD 258
Db 236 ETAILKKLDHNVVVKLTVELDDPAEDNLVLFVLLRKGPMVEVPCDKPFEEQARLYLRD 295

QY 259 VIILGLEVLHCQKIVHRDIKPSNLLLDGDDHVKVTADFGVSNQFPGNDAQLSSTAGTAFMA 318
Db 296 LIRGIEYLHYQKIITHRDIKPSNLLLDGDDHVKVTADFGVSNQFPGNDAQLSSTAGTAFMA 355

QY 319 PEALSDSGSQSGKALDVMATGVTLYCFVYKGCFFIDDFTLALHRIKNEPVVFPPEPEI 378
Db 356 PESLSETRKIFSGKALDVMATGVTLYCFVYKGCFFIDDFTLALHRIKNEPVVFPPEPEI 415
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QY 379 SEELKDLILKMLDKNPETRIGVDPDIKLHPMTXNGEPLPSEBEHCSVWVTEGEVKNV 438
Db 416 AEDLKDLITRMKLNKRPESRIVVPEIKLHPMTXNGEPLPSEBEHCSVWVTEGEVKNV 475

QY 439 RLIPSWTTVILVKSMRLKRSFGNPFEPQARREERSMSAPGNLLIKQVSEVAKSDLPDVE 498
Db 476 KHIPSLATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLIKQVSEVAKSDLPDVE 534

QY 499 QEDE 502
Db 535 GEEE 538

RESULT 9
Q8IU03 PRELIMINARY; PRT; 541 AA.
AC Q8IU03;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ca2+/calmodulin-dependent protein kinase kinase beta-3.
DE CAMKK BETA-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishikawa Y., Tokumitsu H., Inuzuka H., Murata-Hori M., Hosoya H.,
RA Kobayashi R.;
RT "Identification and characterization of novel components of
RT Ca2+/calmodulin-dependent protein kinase cascade in HeLa cells.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391903; PubMed=11395482;
RA Hsu L.-S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT "Human Ca2+/calmodulin-dependent protein kinase kinase beta gene
RT encodes multiple isoforms that display distinct kinase activity.";
RL J. Biol. Chem. 276:31113-31123 (2001).
DR EMBL; AB081336; BAC19840.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Kinase.
SQ SEQUENCE 541 AA; 59601 MW; D9A56C3D780C0DDE CRC64;

Query Match 58.3%; Score 1536; DB 4; Length 541;
Best Local Similarity 65.1%; Pred. No. 8.1e-116;
Matches 293; Conservative 77; Mismatches 68; Indels 12; Gaps 3;

QY 64 ARPSLSARKLSLQER-----PAGSYLQAG-----PYATGPASHISPRAWRPPTIESH 112
Db 90 ARPHLSGRKLSLQERSQGLAGGSLDMNGRCICPLSPYSPVSSPSSPSSPSSPSSPSSPSS 149

QY 113 HVAISDAEDCVQLNKLQSEIGKGA YGVVRLAYNESEDRHYAMKVLKSKLLKQYGFRR 172
Db 150 HVSITGMQDCVQLNQLTKLDEIGKSGYGVVKKLAYNENDNTYYAMKVLKSKLLKQYGFRR 209

QY 173 RPPPRGSAQAGGAPAKQLPLSERVYQETAILKKLDHNVVVKLTVELDDPAEDNLVLFV 232
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Query Match 57.9%; Score 1525; DB 11; Length 541;
Best Local Similarity 60.1%; Pred. No. 6.3e-115;
Matches 300; Conservative 79; Mismatches 70; Indels 50; Gaps 7;
SQ SEQUENCE 533 AA; 5885 MW; 55B930B6EE4B678D CRC64;

QY 36 EPTRENGV-----DPPPRARAASVIFGSTRRLP-----ARPSLSARKLSLQERPAGS 82
DB 58 EPGR-GVDNLNLRDQPEA-----DQELPLEASDPESRSPLSGRKWSLQE----- 102
QY 83 YLEAQAAGP-----YATGPASHISPRAWRPPTIESHVHVAISDAEDCV 123
DB 103 --PSOGGPASSNSLDMNGRCICPSLSYSPASSPQSSPRMPRPPTVESHHSVITGLQDCV 160
QY 124 QLNQYKLSQSIGKAGYGVVRLAYNESDRHYAMKVLKSKLLKQYGFPRPPRPGSQAQ 183
DB 161 QLNQYTLKDDIGKSGYGVVRLAYNENDNTYYAMKVLKSKLLKQYGFPRPPRPGAPAP 220
QY 184 GGPAKQLPLERYVQETAILKLDHNVVVKLIEVLDDPAEDNLYLVFDLLKRGVMEVPC 243
DB 221 GGCIQPRGPTEVQYETAILKLDHNVVVKLIEVLDDPAEDNLYLVFDLLKRGVMEVPT 280
QY 244 DKPFSEQARLYLRDVLGLYHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQPEGN 303
DB 281 LKPLSDQARFYQDLTKGTEYLYHQKIIHRDIKPSNLLGDDGHVKIADFGVSNQPEGN 340
QY 304 DAQLSSTAGTAPAFWAPPAISDSGQSPSKALDVWATGVTLYCFVYKCPIDDFILALHR 363
DB 341 DALLSNVGTAPAFWAPPAISDSGQSPSKALDVWATGVTLYCFVYKCPIDDFILALHR 400
QY 364 KIRNEPVVPEEPEISBELKDLILKMLDKNPETRIGVDPDKLHPWTKNGEELPSEEH 423
DB 401 KIRSALEFPDQDIAEDLKDLITMLDKNPESRIVVPEIKLHPWTRHGAELPSEDEN 460
QY 424 CSVVETEGVKNSVRLIPSWTVVILVKSMLRKSFGNPPQARREERSMSAPGNLLVK 483
DB 461 CTIVETEEVENSVKHSPLATVILVKTMRKSFNPFPGFSGRREERSMSAPGNLLTK 519
QY 484 EGFEGGKSPELPGVQDE 502
DB 520 QGSEDSRGPPEAPVGEZ 538

RESULT 12

Q96RR3 PRELIMINARY; PRT; 533 AA.
AC Q96RR3; ID Q96RR3; PRELIMINARY; PRT; 533 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase b2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391903; PubMed=11395482;
RA Hsu L.S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT "Human Ca2+/Calmodulin-dependent Protein Kinase beta Gene
RT Encodes Multiple Isoforms That Display Distinct Kinase Activity.";
RJ. J. Biol. Chem. 276:31113-31123(2001).
CC -/- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF287631; AAK64601.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR008271; Ser Thr pkinase.
DR Pfam; PF00069; pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

RESULT 13

Q96RR4 PRELIMINARY; PRT; 588 AA.
AC Q96RR4; ID Q96RR4; PRELIMINARY; PRT; 588 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase b1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391903; PubMed=11395482;
RA Hsu L.S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT "Human Ca2+/Calmodulin-dependent Protein Kinase beta Gene
RT Encodes Multiple Isoforms That Display Distinct Kinase Activity.";
RJ. J. Biol. Chem. 276:31113-31123(2001).
CC -/- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF287630; AAK64600.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR008271; Ser Thr pkinase.
DR Pfam; PF00069; pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.

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DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 588 AA; 64731 MW; D4C4583561341166 CRC64;

Query Match
Best Local Similarity 57.6%; Score 1518.5; DB 4; Length 588;
Matches 295; Conservative 75; Mismatches 65; Indels 31; Gaps 5;

QY 30 EADGQPEPTRNGVDPPPRARAASVTPGSTSRLLPAPSLSSARKLSQER-----PAGSVYL 84
DB 75 EADGQEP-----LDSSGQ---ARPHLSGRKLSQERSQGLAAGSL 115
QY 85 EAQAG-----PYATGPASHISPRAWRPTTIESHVAISDAEDCVQLNQYKLSQSEIGKA 138
DB 116 DMNGRCICPSLPSPVSSPSSPRLPRPTVESHHVSIITGMQDCVQLNQYTLKDEIGKGS 175
QY 139 YGVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSOAAQGGPAKQLPLERVYQ 198
DB 176 YGVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSOAAQGGPAKQLPLERVYQ 235
QY 199 EIALKLLDHPNVKLVLEVDPAEDNLVLFDDLRKGPVMEVPCDKPFSEQARLYLRD 258
DB 236 EIALKLLDHPNVKLVLEVDPAEDNLVLFDDLRKGPVMEVPCDKPFSEQARLYLRD 295
QY 259 VILGLEYLHCQKIVHRDIKPSNLLGDDGHVFIADFGVSNQFEGNDAQLSSTAGTAPFMA 318
DB 296 LKIGIEYLHYQKIHRDIKPSNLLGDDGHVFIADFGVSNQFEGNDAQLSSTAGTAPFMA 355
QY 319 PRAISDSGSGSKALDVWATGTYLCFYVYKCPFDIDFIALHRKIKNEPVVFPPEEI 378
DB 356 PPSLSSTRKIFSGKALDVWATGTYLCFYVYKCPFDIDFIALHRKIKNEPVVFPPEEI 415
QY 379 SEELKDLILKMLDKXNPETRIQVDPDKLHPWTKNGEPLPSPEEHCSSVVEVTEGEVNSV 438
DB 416 AEDLKDLITRLMDKXNPESILVPEIKLHPWTRHGAELPLPSDENCTLVETVEEVEVNSV 475
QY 439 RLIPSWTIVLVKSMRLKRSFGNPFEPQARRERSMSAPGNLLVKE 484
DB 476 KHIPSLATVILVTKMIRKRSFGNPFEPQARRERSMSAPGNLLVKE 520

RESULT 14
Q96RP2 PRELIMINARY; PRT; 533 AA.
AC Q96RP2;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Ca2+/calmodulin-dependent protein kinase beta 2.
GN CAMK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391903; PubMed=11395482;
RA Hsu L.S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT "Human Ca2+/Calmodulin-dependent Protein Kinase beta Gene
RT Encodes Multiple Isoforms That Display Distinct Kinase Activity.";
RL J. Biol. Chem. 276:31113-31123 (2001).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF321401; AAK91830.1; JOINED.
DR EMBL; AF321390; AAK91830.1; JOINED.
DR EMBL; AF321575; AAK91830.1; JOINED.
DR EMBL; AF321391; AAK91830.1; JOINED.
DR EMBL; AF321392; AAK91830.1; JOINED.
DR EMBL; AF321393; AAK91830.1; JOINED.
DR EMBL; AF321576; AAK91830.1; JOINED.
DR EMBL; AF321577; AAK91830.1; JOINED.
DR EMBL; AF321394; AAK91830.1; JOINED.

DR EMBL; AF321395; AAK91830.1; JOINED.
DR EMBL; AF321396; AAK91830.1; JOINED.
DR EMBL; AF321397; AAK91830.1; JOINED.
DR EMBL; AF321398; AAK91830.1; JOINED.
DR EMBL; AF321399; AAK91830.1; JOINED.
DR EMBL; AF321400; AAK91830.1; JOINED.
DR EMBL; AF321578; AAK91830.1; JOINED.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006468; P:protein kinase activity; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 533 AA; 58899 MW; 98FAAB0FB8C4CACF CRC64;

Query Match
Best Local Similarity 57.6%; Score 1517; DB 4; Length 533;
Matches 288; Conservative 73; Mismatches 59; Indels 12; Gaps 3;

QY 64 ARPSLSARKLSQER-----PAGSVLEAQG-----PYATGPASHISPRAWRPTTIESH 112
DB 90 ARPHLSGRKLSQERSQGLAAGSLDMNGRCICPSLPSPVSSPSSPRLPRPTVESH 149
QY 113 HVAISDAEDCVQLNQYKLSQSEIGKAGYGVVRLAYNESEDRHYAMKVLKKLLKQYGFPR 172
DB 150 HVSITGMQDCVQLNQYTLKDEIGKSGYGVVRLAYNESEDRHYAMKVLKKLLKQYGFPR 209
QY 173 RPPRGSOAAQGGPAKQLPLERVYQETAILKLDHPNVVVKLVLEVDPAEDNLVLFDL 232
DB 210 RPPRGTRTPAPGGCIQPRGPIEQVYQETAILKLDHPNVVVKLVLEVDPAEDNLVLFDL 269
QY 233 LRKGPVMEVPCDKPFSEQARLYLRDVLGLBYLHCQKIVHRDIKPSNLLGDDGHVKA 292
DB 270 VNQGPVMEVPTLKLPSLSEDAQRYFDLKGILYHQIKLHRDIKPSNLLGDDGHVKA 329
QY 293 DFGVSNQFEGNDAQLSSTAGTAPFMAPEAISDSGSGSKALDVWATGTYLCFYVYKCP 352
DB 330 DFGVSNQFEGNDAQLSSTAGTAPFMAPEAISDSGSGSKALDVWATGTYLCFYVYKCP 389
QY 353 FIDDEILALHRKIKNEPVVFPPEEPISEELKDLILKMLDKXNPETRIQVDPDKLHPWTKN 412
DB 390 FMDEIMCLHSKIKSQAELFPDQDIAEDKDLITRLMDKXNPESILVPEIKLHPWTRH 449
QY 413 GEEPLPSEEEHCSSVVEVTEGEVNSVRLIPSWTIVLVKSMRLKRSFGNPFEPQARRER 472
DB 450 GAPELPSDENCTLVETVEEVEVNSVRLIPSWTIVLVKSMRLKRSFGNPFEPQARRER 508
QY 473 SMSAPGNLLVKE 484
DB 509 SILSAPGNLLTKK 520

RESULT 15
Q96RP1 PRELIMINARY; PRT; 588 AA.
AC Q96RP1;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Ca2+/calmodulin-dependent protein kinase beta 1.
GN CAMK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21391903; PubMed=11395482;
RA  Hsu L.S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT  "Human Ca2+/Calmodulin-dependent Protein Kinase beta Gene
RT  Encodes Multiple Isoforms That Display Distinct Kinase Activity.";
RL  J. Biol. Chem. 276:31113-31123 (2001).
CC  -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR  EMBL; AF321402; AAK91829.1;
DR  EMBL; AF321390; AAK91829.1; JOINED.
DR  EMBL; AF321575; AAK91829.1; JOINED.
DR  EMBL; AF321391; AAK91829.1; JOINED.
DR  EMBL; AF321392; AAK91829.1; JOINED.
DR  EMBL; AF321393; AAK91829.1; JOINED.
DR  EMBL; AF321576; AAK91829.1; JOINED.
DR  EMBL; AF321577; AAK91829.1; JOINED.
DR  EMBL; AF321394; AAK91829.1; JOINED.
DR  EMBL; AF321395; AAK91829.1; JOINED.
DR  EMBL; AF321396; AAK91829.1; JOINED.
DR  EMBL; AF321397; AAK91829.1; JOINED.
DR  EMBL; AF321398; AAK91829.1; JOINED.
DR  EMBL; AF321399; AAK91829.1; JOINED.
DR  EMBL; AF321400; AAK91829.1; JOINED.
DR  EMBL; AF321578; AAK91829.1; JOINED.
DR  Genew; HGNC:1470; CAMKK2.
DR  GO; GO:000524; F:ATP binding; IEA.
DR  GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR  GO; GO:0016740; F:transferase activity; IEA.
DR  GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR002290; Ser_thr_pkin_AS.
DR  Pfam; PF00069; pkinase; 1.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00220; S_TK; 1.
DR  PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR  PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR  PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW  ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ  SEQUENCE 588 AA; 64769 MW; B1F714C6AE04117A CRC64;

Query Match      57.6%; Score 1517; DB 4; Length 588;
Best Local Similarity 66.7%; Pred. No. 3.2e-114;
Matches 288; Conservative 73; Mismatches 59; Indels 12; Gaps 3;

QY  64 ARPSLSARKLSLQSR-----PAGSYLEAQAG-----PYATGPASHISPRARRPTTIESH 112
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  90 ARPHLSGRKLSLQSRSGGLAAGSLDMNGRCICPSLPYSPVSPQSSPRLPRPTVESH 149
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  113 HVAISDAEDCVQLNQYKLSQSEIGKYGAVVRLAYNESEDRHYAMKVLKSKLLKQYGFPR 172
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  150 HVSITGMQDCVQLNQYTLKDEIGKSGVGVKLYNENDNTYYAMKVLKSKLLIRQAGFPR 209
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  173 RPPRGSQAAGGPAKQLPLERYQYQIALKKLDHVNVMVKLIEVLDDPAEDNLYLVFDL 232
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  210 RPPRGTTRPAGGCIQPRGPIEQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 269
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  233 LRKGPVMEVFCDFSEQARLYLRDVLGLVYLHCOKIVHRDIKPSNLLIGDDGHVKIA 292
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  270 VNOGPMVEVPTLPLSSEDQARFVQDLIKGIEYLYHQYKIHROIKPSNLLVGEDGHKIA 329
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  293 DFGVSNQFEGNDAQLSCTAGTPAPMAPEAISDSQSPSGKALDVWATGVTLVCFVYGKCP 352
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  330 DFGVSNFEFGKSDALLSNVTGTPAPMAPELSLSETRKIFSGKALDVWANGVTLYCFVFGCP 389
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  353 FIDFIALHRKIKNEPVFPPEPEISEELKDLIKMLDKNPETRIGVPOIKLHPWVTYN 412
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  390 FMDERIMCLSHKSKSQALEFPDQDIAEDLKDILTRMLDKNPESRIVVVPEIKLHPWVTRH 449
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  413 GEELPSEERHKSQVVEYTEGVEKNSVRLIPSTVTTVILVSKMLRKRSFGNPEPQARRER 472
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  450 GAELPSEDENCILVETEEVENSVKHIFSLATVILVKTMRKRSFGNPFPE-GSRREER 508
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY  473 SMSAPGNLLVKE 484
DB  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  509 SLSAPGNLLTRK 520
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Search completed: July 12, 2004, 04:52:55
Job time : 90 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	2190	100.0	2190	14	US-10-135-689-1	Sequence 1, Appli
2	2190	100.0	2190	17	US-10-690-617-1	Sequence 1, Appli
3	2001.6	91.4	3501	13	US-10-168-582-14	Sequence 14, Appli
4	1906.4	87.1	1937	13	US-10-333-314-39	Sequence 39, Appli
5	1636.2	74.7	2711	9	US-09-923-118-7	Sequence 7, Appli
6	1636.2	74.7	2711	17	US-10-391-364-41	Sequence 41, Appli
7	1610.2	73.5	2018	13	US-10-302-172-433	Sequence 43, App
8	1601.4	73.1	1611	13	US-10-082-900A-55	Sequence 55, Appli
9	1493.8	68.2	1547	13	US-10-082-900A-53	Sequence 53, Appli
10	1490.6	68.1	1683	9	US-09-928-138-9	Sequence 9, Appli
11	1490.6	68.1	1686	17	US-10-391-364-43	Sequence 43, Appli
12	1475.8	67.4	1725	13	US-10-092-900A-57	Sequence 57, Appli
13	653.6	29.8	5611	16	US-10-295-027-1138	Sequence 1138, Ap
14	651.2	29.7	4427	15	US-10-316-124-7	Sequence 7, Appli

Qy 121 GGCGCCAGGTTCCCAACAAGGCTA

	Query Match	100.0%;	Score 2190;	DB 14;	Length 2190;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2190;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	CGCCCGCGGGCTGAGCTCGGGGATCTGGGCCCCAGCGAGCGGTGGGGCGGGCGGGCGG	60		
Db	1	CGCCCGCGGGGTGAGCTCGGGCGATCTGGGCCCCAGCGAGCGGTGGGGCGGGCGGGCGG	60		
QY	61	GGGCGGGGCGCGCAGCAGGAGCGAGTGGGCGCGCCCGCGGGGCCACGGACACTGTGCGCC	120		
Db	61	GGGCGGGGCGCGCAGCAGGAGCGAGTGGGCGCGCCCGCGGGGCCACGGACACTGTGCGCC	120		
QY	121	GGCGCCCGAGGTTTCCACACAGGGCTACGCAGAGAAGCCCCCTTGACTGAAGCAATGGAGG	180		

Db 121 GGGGCCCGAGGTTCCCAACAAGGCTACGAGAGAACCCCTTGACTGAGCAATGGAGGG 180
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Db 181 GGGTCCAGCTGTCTGTGCCAGGATCTCTGGGAGAGCTGGTAGAAGGGGTGGCAGCCAT 240
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Db 301 CCCCCACACAGGCGCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCC 360
QY 361 AGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGAGCGGCCAGCAGGAAGCTA 420
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Db 661 GTTACTGAAGCAGTATGGCTTTCACAGTGCCTCCCGAGAGGGTCCAGGCTGCCCA 720
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QY 841 GGACAACTCTATTTGGTGTGGTCTCTGAGAAAGGGGCCCGTCAATGAAAGTGGCCTG 900
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QY 961 CGAGTACTTGCACTGCCAGAAAGTCTGTCACAGGACATCAAGCCATCCAACTGCTCCT 1020
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QY 1021 GGGGGATGATGGGCACTGTAAGATTCGCGACTTTGGCGTCAAGCAACAGTTTGAAGGGAA 1080
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QY 1381 CAAGTTGCACCCCTTGGGTGACCAAGAACGGGAGGAGCCCTCTCTTCGGAGGAGGAGCA 1440
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QY 1441 CTGAGCGTGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAAGGCTCATCCCCAG 1500
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QY 1501 CTGAGCACCGTGTATCCTGTGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAACCCGTT 1560
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QY 1561 TGAGCCCCAGGCAAGGAGGAGGATCCATGTCTGTCTCAGGAAACCTACTGTGTAA 1620
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QY 1621 AGAAGGTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGGGTTCAGGAAGCAGGCG 1680
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QY 1681 TGATCTGAGCCCTCTCATGCAAGGAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
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QY 2041 GGCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
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QY 2101 TGCGTCACTGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
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QY 2161 GGCACACAGAGCTCTTGTCTATTCAGACGCT 2190
Db 2161 GGCACACAGAGCTCTTGTCTATTCAGACGCT 2190

RESULT 2
US-10-690-617-1
; Sequence 1, Application US/10690617
; Publication No. US20040086926A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEROPF
; FILE REFERENCE: CL000904DIV II
; CURRENT APPLICATION NUMBER: US/10/690,617
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-690-617-1

Query Match 100.0%; Score 2190; DB 17; Length 2190;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1681 TGCACTCTGAGCCCTGCACTGCAACAGGCGCACCCGAGCAGACACTCATCCCGGCTC 1740
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QY 1459 TTCTTTGGAGGAGGAGCACTGACAGCGTGTGTGAGGTGACAGAGGGGGAGTTAAGAACTC 1518
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QY 1783 GGGCTGGGAGCTGCAGGCCCACTCCCGCCCTCCCGCCCTCATGCGTCATGACTCCACGC 1842
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QY 1699 GGGCTGGGAGCTGCAGGCCCACTCCCGCCCTCCCGCCCTCATGCGTCATGACTCCACGC 1758
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QY 1843 ACGCAGCTCCAGGAGCAGACGTGAATGTATGTCATTTGGGGTCTTGGGGGAGGAGGCTCCC 1902
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QY 1759 ACGCAGCTCCAGGAGCAGACGTGAATGTATGTCATTTGGGGTCTTGGGGGAGGAGGCTCCC 1818
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QY 1963 GTGCCATGGAGCTTCAGAAATGCCACCGGCTGTGGCATGGCTGGGGGAGGAGCA 2022
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QY 2023 GAGCAGAGACCAAGATGGCAGGTGGAGGCGAGGCTTACCAACAGGAAGAGCTCCC 2082
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RESULT 4
US-10-333-314-39
; Sequence 39, Application US/10333314
; Publication No. US20030211093A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
; APPLICANT: HAFALIA, April J.A.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Javalaxmi
; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.
; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAL, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
```

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; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0162 USN
; CURRENT APPLICATION NUMBER: US/10/333,314
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: PCT/US01/23092
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,038
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/222,112
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,831
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,729
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 39
; LENGTH: 1937
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2190612CB1
US-10-333-314-39

Query Match 87.1%; Score 1906.4; DB 13; Length 1937;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 250 TCATTGGAGGAGGAGATGTTGGCCAGAGCTTACTAGAAAACGGTGTGGACCCGCCACC 309
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QY 142 TCATTGGAGGAGGAGATGTTGGCCAGAGCTTACTAGAAAACGGTGTGGACCCGCCACC 201
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QY 310 ACGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCC 369
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QY 202 ACGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCC 261
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QY 370 TAGCCTCTCAGCCAGGAAGCTTTCCCTACAGAGCGGCCAGCAGGAAGCTATCTGGAGGC 429
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Db 573 AACCACTAAGCTGCAAGTGCAGATGAGATTGCAAGGGTGCCTACGGTGTGTGAGGCTGGCC 632
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QY 788 CTGACCAAGCTGAATGTGCTCAAACTGATCGAGGTCCTGATGACCCAGCTCAGAGCAAC 847
Db 813 CTGACCAAGCTGAATGTGCTCAAACTGATCGAGGTCCTGATGACCCAGCTCAGAGCAAC 872
QY 848 CTCTATTTGCTTTGAACTCTCTGAAAGGGCCCGTCATGAAAGTGCCCTGTGACAAAG 907
Db 873 CTCTATTTGCTTTGAACTCTCTGAAAGGGCCCGTCATGAAAGTGCCCTGTGACAAAG 932
QY 908 CCCTTCTCGGAGGACAGCTGCTGCTCTACCTGCGGAGCTCATCTGGGCTCAGAGTAC 967
Db 933 CCCTTCTCGGAGGACAGCTGCTGCTCTACCTGCGGAGCTCATCTGGGCTCAGAGTAC 992
QY 968 TTGCACTGCCAAGATCGTCCACAGGACATCAAGCCATCAAGCTGCTCTCGGGGAT 1027
Db 993 TTGCACTGCCAAGATCGTCCACAGGACATCAAGCCATCAAGCTGCTCTCGGGGAT 1052
QY 1028 GATGGGCAAGTGAAGTCCGCACTTTGGCGTCAAGCAACCAAGTTTGGGGGAAACGACGT 1087
Db 1053 GATGGGCAAGTGAAGTCCGCACTTTGGCGTCAAGCAACCAAGTTTGGGGGAAACGACGT 1112
QY 1088 CAGCTGTCCAGCAGCGGGGAAACCCAGCATTCATGGGCCACTGGGCTCACGTTGTACTGTC 1147
Db 1113 CAGCTGTCCAGCAGCGGGGAAACCCAGCATTCATGGGCCACTGGGCTCACGTTGTACTGTC 1172
QY 1148 GGCAGAGCTTCAGTGGGAAAGCCCTTTGGATGATGGGCCACTGGGCTCACGTTGTACTGTC 1207
Db 1173 GGCAGAGCTTCAGTGGGAAAGCCCTTTGGATGATGGGCCACTGGGCTCACGTTGTACTGTC 1232
QY 1208 TTTGTCTAAGGAGTGCCTTCAATCAACGATTTTCATCTGGCCCTCCACAGGAAGATC 1267
Db 1233 TTTGTCTAAGGAGTGCCTTCAATCAACGATTTTCATCTGGCCCTCCACAGGAAGATC 1292
QY 1268 AAGATGAGCCGCTGCTGTTCTCTGAGGAGCCAGAAATCAGGAGGAGCTCAAGACCTG 1327
Db 1293 AAGATGAGCCGCTGCTGTTCTCTGAGGAGCCAGAAATCAGGAGGAGCTCAAGACCTG 1352
QY 1328 ATCTCTGAAGATGTTAGACAAGAAATCCGAGAGGAAATTTGGGTGCCAGACATCAAGTTG 1387
Db 1353 ATCTCTGAAGATGTTAGACAAGAAATCCGAGAGGAAATTTGGGTGCCAGACATCAAGTTG 1412
QY 1388 CACCTTTGGGTGAACAAGAACGGGAGGAGCCCTTCTCTCGGAGGAGGAGCACTGCAGC 1447
Db 1413 CACCTTTGGGTGAACAAGAACGGGAGGAGCCCTTCTCTCGGAGGAGGAGCACTGCAGC 1472
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QY 1448 GTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCAGCTGGACC 1507
Db 1473 GTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCAGCTGGACC 1532
QY 1508 ACGETGATCTCGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAAACCGGTTTGAGCCC 1567
Db 1533 ACGETGATCTCGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAAACCGGTTTGAGCCC 1592
QY 1568 CAGGACCGGAGGGAAGAGCGATCCATGCTCTCCAGGAAACCTACTGCTGGAAGAGGG 1627
Db 1593 CAAGCACGAGGGAAGAGCGATCCATGCTCTCCAGGAAACCTACTGCTGGAAGAGGG 1652
QY 1628 TTTGTGAAAGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGGAAGACGA 1677
Db 1653 TTTGTGAAAGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGGCTTACCA 1702
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RESULT 6

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US-10-391-364-41
; Sequence 41, Application US/10391364
; Publication No. US20040121349A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Cook, William James
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Welch, Nadine S.
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352,
; TITLE OF INVENTION: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: MPI03-0190NMIM
; CURRENT APPLICATION NUMBER: US/10/391,364
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/950,370
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/231,084
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 10/294,039
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/338,587
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 10/266,035
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US 60/328,198
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/717,926
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/214,707
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 10/268,036
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/327,820
; PRIOR FILING DATE: 2001-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 2711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (198)...(1883)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2711)
; OTHER INFORMATION: n = A,T,C or G
US-10-391-364-41
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Query Match

Best Local Similarity 74.7%; Score 1636.2; DB 17; Length 2711;

98.9%; Pred. No. 0;

Matches 1652; Conservative 4; Mismatches 13; Indels 1; Gaps 1;			
QY	8	GGGCTGAGCTCGCGATCTGGGCCCCAGAGCGGTGGGCGGGCGGGCGGGCGGG	67
Db	34	GGGCTGNGCTC SRGWTYCGGTCGCCCCAGCGAGCGGTGGGCGGGCGGGCGGGCGGG	93
QY	68	GGCGGACGAGGAGCGAGTGGGCGCGCCCGCGGCGCCAGGACACGTGTGCCCGGGCCC	127
Db	94	GGCGGACGAGGAGCGAGTGGGCGCG - CGCGCGGCGCGCGGACACTGTGCCCGGGCCC	152
QY	128	AGGTTCCCAACAGGCTTACCGAGAAACCCCTTGACTGAAGCAATGGAGGGGGTCCA	187
Db	153	AGGTTCCCAACAGGCTTACCGAGAAACCCCTTGACTGAAGCAATGGAGGGGGTCCA	212
QY	188	GCTGTCTGCTGCCAGGATCTCGGGCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTG	247
Db	213	GCTGTCTGCTGCCAGGATCTCGGGCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTG	272
QY	248	ACTCACTTGAGGAGGAGATGGTGGCCAGAGCCTACTAGAACGGGTGGACCCGCCA	307
Db	273	ACTCACTTGAGGAGGAGATGGTGGCCAGAGCCTACTAGAACGGGTGGACCCGCCA	332
QY	308	CCACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGG	367
Db	333	CCACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGG	392
QY	368	CCTAGCCTCAGCCAGGAAGCTTTCCTACAGAGCGGCCAGCAGGAAGCTATCTGGAG	427
Db	393	CCTAGCCTCAGCCAGGAAGCTTTCCTACAGAGCGGCCAGCAGGAAGCTATCTGGAG	452
QY	428	GGCGAGGCTGGGCTTATGCCAGGGGCTGCCAGCCACATCTCCCCGGGCTGCGG	487
Db	453	GGCGAGGCTGGGCTTATGCCAGGGGCTGCCAGCCACATCTCCCCGGGCTGCGG	512
QY	488	AGGCCCAACCATCGAGTCCCAACAGTGGCCATCTCAGATGACAGGACTGCTGACGCTG	547
Db	513	AGGCCCAACCATCGAGTCCCAACAGTGGCCATCTCAGATGACAGGACTGCTGACGCTG	572
QY	548	AACCACTACAGCTGACAGTGAATGGGACAGGGTCTACGGTGTGGTGAAGCTGGCC	607
Db	573	AACCACTACAGCTGACAGTGAATGGGACAGGGTCTACGGTGTGGTGAAGCTGGCC	632
QY	608	TACAACCAAGTGAAGCAGACACTATGCAATGAAGTCTTTCACAAAGAAAGTACTG	667
Db	633	TACAACCAAGTGAAGCAGACACTATGCAATGAAGTCTTTCACAAAGAAAGTACTG	692
QY	668	AAGCAGTATGGCTTTCCACGTCGCGCTCCCCCGAGAGGTTCCAGGCTGCCAGGAGGA	727
Db	693	AAGCAGTATGGCTTTCCACGTCGCGCTCCCCCGAGAGGTTCCAGGCTGCCAGGAGGA	752
QY	728	CCAGCCAGCAGCTGCTGCCCTGGAGCGGGTGTACAGAGAGATGCCATCTGAAGAG	787
Db	753	CCAGCCAGCAGCTGCTGCCCTGGAGCGGGTGTACAGAGAGATGCCATCTGAAGAG	812
QY	788	CTGACCAACGTAATGTGGTCAAACTGATCGAGTCTCTGGATGACCCAGCTGAGACAAC	847
Db	813	CTGACCAACGTAATGTGGTCAAACTGATCGAGTCTCTGGATGACCCAGCTGAGACAAC	872
QY	848	CTCTATTGTGTTGACCTCTGAGAAAGGGGCCGCTCATGGAAGTGCCTGTGACAAG	907
Db	873	CTCTATTGTGTTGACCTCTGAGAAAGGGGCCGCTCATGGAAGTGCCTGTGACAAG	932
QY	908	CCCTTCTCGGAGGACAGCTCGCTCTACTCGGGGACGTCATCTGGGCTCGAGTAC	967
Db	933	CCCTTCTCGGAGGACAGCTCGCTCTACTCGGGGACGTCATCTGGGCTCGAGTAC	992
QY	968	TTGACCTCCAGAGATCGTCCACAGGACATCAAGCCATCCAACTCTCTCTGGGGAT	1027
Db	993	TTGACCTCCAGAGATCGTCCACAGGACATCAAGCCATCCAACTCTCTCTGGGGAT	1052
QY	1028	GATGGGACGTGAAGATCGCCGACTTTGGCGTCAAGAACCAAGTTTGGGGAAACGACGCT	1087
Db	1053	GATGGGACGTGAAGATCGCCGACTTTGGCGTCAAGAACCAAGTTTGGGGAAACGACGCT	1112

QY	1088	CAGCTCTCAGACACGGCGGAACCCAGCATTCATGSCCCCCGAGGCCATTTCTGATTCC	1147
Db	1113	CAGCTCTCAGACACGGCGGAACCCAGCATTCATGSCCCCCGAGGCCATTTCTGATTCC	1172
QY	1148	GGCCAGAGCTTCAGTGGGAGGCGCTTGGATGTATGGGCCACTGGCGCTCACGTTGTACTGC	1207
Db	1173	GGCCAGAGCTTCAGTGGGAGGCGCTTGGATGTATGGGCCACTGGCGCTCACGTTGTACTGC	1232
QY	1208	TTTGTCTATGGGAAGTGCCTCATTCATCGACGATTTTCTGCGCCCTCCACAGGAAGATC	1267
Db	1233	TTTGTCTATGGGAAGTGCCTCATTCATCGACGATTTTCTGCGCCCTCCACAGGAAGATC	1292
QY	1268	AAGAAATGAGCCCTGGTGTCTCTGAGGAGCAGAAATCAGCCAGGAGCTCAAGGACCTG	1327
Db	1293	AAGAAATGAGCCCTGGTGTCTCTGAGGAGCAGAAATCAGCCAGGAGCTCAAGGACCTG	1352
QY	1328	ATCCTGAAGATGTTAGACAGAAATCCCGAGACAGAAATTTGGGTGCCAGACATCAAGTTG	1387
Db	1353	ATCCTGAAGATGTTAGACAGAAATCCCGAGACAGAAATTTGGGTGCCAGACATCAAGTTG	1412
QY	1388	CACCTTTGGTGACCAAGAAACGGGAGGAGCCCTTCTTCCGAGGAGGAGCACTGCAGC	1447
Db	1413	CACCTTTGGTGACCAAGAAACGGGAGGAGCCCTTCTTCCGAGGAGGAGCACTGCAGC	1472
QY	1448	GTGCTGAGGTGACAGAGGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACC	1507
Db	1473	GTGCTGAGGTGACAGAGGAGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACC	1532
QY	1508	ACGCTGATCTCTGGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAACCCGTTTGAGCCC	1567
Db	1533	ACGCTGATCTCTGGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAACCCGTTTGAGCCC	1592
QY	1568	CAGCAGCAGGAGGAGGAGCCATCCATGCTCTGCTCCAGGAACCTTACTGCTGAAGAAGGG	1627
Db	1593	CAAGCAGCAGGAGGAGGAGCCATGCTCTGCTCCAGGAACCTTACTGCTGAAGAAGGG	1652
QY	1628	TTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGCGCTCCAGGAAGACGA	1677
Db	1653	TTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGCGCTCCAGGAAGACGA	1702

RESULT 7

US-10-302-172-433
; Sequence 433, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids a
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803_1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 433_
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1746)
US-10-302-172-433

Query Match

73.5%; Score 1610.2; DB 13; Length 2018;

Best Local Similarity 98.3%; Pred. No. 0;					Matches 1638; Conservative 0; Mismatches 28; Indels 1; Gaps 1;				
QY	129	GGTTCCCAACAGGCTACGACAGAAACCCCTTGACTGAAGCAATGAGGGGGTCCAG	188						
Db	188	GGTTCCCAACAGGCTACGACAGAAACCCCTTGACTGAAGCAATGAGGGGGTCCAG	247						
QY	189	CTGTCTGTCTGCGAGAGTCTTGGGAGAGCTGGTAGAAACGGGTGACGCCATTCGATGTGA	248						
Db	248	CTGTCTGTCTGCGAGAGTCTTGGGAGAGCTGGTAGAAACGGGTGACGCCATTCGATGTGA	307						
QY	249	CTCACTTGGAGAGGACAGATGCTGSCCCAGAGCCTACTAGAAAACGGTGTGACCCCCAC	308						
Db	308	CTCACTTGGAGAGGACAGATGCTGSCCCAGAGCCTACTAGAAAACGGTGTGACCCCCAC	367						
QY	309	CACGGGCCAGAGCTGCTCTGTGTATCCCTGGCAGTACTTCAAGACTGTCTCCAGCCCGC	368						
Db	368	CACGGGCCAGAGCTGCTCTGTGTATCCCTGGCAGTACTTCAAGACTGTCTCCAGCCCGC	427						
QY	369	CTAGGCTCTACGCCAGGAAGCTTTCCCTACAGGAGCGCCAGAGGAAGCTATCTGGAGG	428						
Db	428	CTAGGCTCTACGCCAGGAAGCTTTCCCTACAGGAGCGCCAGAGGAAGCTATCTGGAGG	487						
QY	429	CGCAGGCTGGCCCTTATSCCAACGGGGCTGCCAGCCACATCTCCCGCGGGCCTGGCGGA	488						
Db	488	CGCAGGCTGGCCCTTATSCCAACGGGGCTGCCAGCCACATCTCCCGCGGGCCTGGCGGA	547						
QY	489	GGCCCCACCATCGAGTCCCAACACGCTGGCCATCTCAGATGCAGAGGACTGCGTGCAGCTGA	548						
Db	548	GGCCCCACCATCGAGTCCCAACACGCTGGCCATCTCAGATGCAGAGGACTGCGTGCAGCTGA	607						
QY	549	ACCACTACAAGTCGACAGTGAATTTGGCAAGGGTGCCCTACGTTGTGTGAGGCTGGGCT	608						
Db	608	ACCACTACAAGTCGACAGTGAATTTGGCAAGGGTGCCCTACGTTGTGTGAGGCTGGGCT	667						
QY	609	ACAAGAAAGTGAAGACAGACATATGCAATGAAGTCTTTTCCAAAAGAAAGTTACTGA	668						
Db	668	ACAAGAAAGTGAAGACAGACATATGCAATGAAGTCTTTTCCAAAAGAAAGTTACTGA	727						
QY	669	AGCAGTATGGCTTTCCAGTCGCGCCCTCCCGGAGAGGGTCCAGGCTCCCGAGGAGGAC	728						
Db	728	AGCAGTATGGCTTTCCAGTCGCGCCCTCCCGGAGAGGGTCCAGGCTCCCGAGGAGGAC	787						
QY	729	CAGCCAGACAGCTGCTGCCCTTGAGAGGGGTGTACAGGAGATTGCCATCTCTGAAGAAGC	788						
Db	788	CAGCCAGACAGCTGCTGCCCTTGAGAGGGGTGTACAGGAGATTGCCATCTCTGAAGAAGC	847						
QY	789	TGGACCAAGTGAATGTGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGAGGACACC	848						
Db	848	TGGACCAAGTGAATGTGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGAGGACACC	907						
QY	849	TCTATTTGGTGTGGTCTGAGAAAGGGGCCCGTCAATGGAAGTGCCTGTGACAAAGC	908						
Db	908	TCTATTTGGTGTGGTCTGAGAAAGGGGCCCGTCAATGGAAGTGCCTGTGACAAAGC	967						
QY	909	CTTTCTGGAGAGCAAGCTGCTCTTACCTGCGGAGCGTCACTCTGGGCCCTCGAGTACT	968						
Db	968	CTTTCTGGAGAGCAAGCTGCTCTTACCTGCGGAGCGTCACTCTGGGCCCTCGAGTACT	1027						
QY	969	TGCACTGCAAGATCGTCCACAGGGACATCAAGCCATCAACTGCTCTCTGGGGGATG	1028						
Db	1028	TGCACTGCAAGATCGTCCACAGGGACATCAAGCCATCAACTGCTCTCTGGGGGATG	1087						
QY	1029	ATGGGACGTGAAGATCGCCGACTTTTGGCGTCAAGCAACAGTGTGAGGGGAACGACGCTC	1088						
Db	1088	ATGGGACGTGAAGATCGCCGACTTTTGGCGTCAAGCAACAGTGTGAGGGGAACGACGCTC	1147						
QY	1089	AGTGTTCAGACGCGGGGAACCCGAGCAATTCATGGCCCCCGAGGCCAATTTCTGATCCG	1148						
Db	1148	AGTGTTCAGACGCGGGGAACCCGAGCAATTCATGGCCCCCGAGGCCAATTTCTGATCCG	1207						
QY	1149	GCCAGAGCTTCAGTGGGAGGCTTGGATGTATGGGCCACTGGGCTCAGCTGTACTGCT	1208						

Db	1208	GCCAGAGCTTCAGTGGGAAGGCGCTTGGATGTATGGGCCACATGGGCCCTCAGTTGTACTGCT	1267						
QY	1209	TTGTCTATGGGAAGTGGCCCATTTTCATCTGGCCCTTCCACAGGAAGATCA	1268						
Db	1268	TTGTCTATGGGAAGTGGCCCGTTCATCGACGATTTTCATCTGGCCCTCCATAGGAAGATCA	1327						
QY	1269	AGATAGAGCCCGTGGTGTCTTCTGAGGAGCCAGAAATCAGCGAGGAGTCAAGGACCTGA	1328						
Db	1328	AGATAGAGCCCGTGGTGTCTTCTGAGGAGCCAGAAATCAGCGAGGAGTCAAGGACCTGA	1387						
QY	1329	TCCTGAGATCTTACAGCAAGAAATCCCGAGAGAGAAATTTGGGGTCCAGACATCAAGTTGC	1388						
Db	1388	TCCTGAGATCTTACAGCAAGAAATCCCGAGAGAGAAATTTGGGGTCCAGACATCAAGTTGC	1447						
QY	1389	ACCTTGGGTGACCAAGAACGGGGAGGAGCCCTTCTTCGAGGAGGAGCACTGCACGG	1448						
Db	1448	ACCTTGGGTGACCAAGAACGGGGAGGAGCCCTTCTTCGAGGAGGAGCACTGCACGG	1507						
QY	1449	TGGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATTCCTCCAGCTGGACCA	1508						
Db	1508	TGGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATTCCTCCAGCTGGACCA	1567						
QY	1509	CGGTGATCTGCTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAAACCGTTTGGAGCCCC	1568						
Db	1568	CGGTGATCTGCTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAAACCGTTTGGAGCCCC	1627						
QY	1569	AGGCACGGAGGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGCTGAAAGAGGGT	1628						
Db	1628	AAGCACGGAGGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGCTGAAAGAGGGT	1687						
QY	1629	TTGTGAAAGGGGGCAAGAGCCAGAGCTCCCGGGTCCAGGAAGAAGAGGCTGATCCT	1688						
Db	1688	TTGTGAAAGGGGGCAAGAGCCAGAGCTCCCGGGTCCAGGAAGAAGAGGCTGATCCT	1747						
QY	1689	GAGCCCTGCAATGACACCCAGGCGCACCCGCGAGACACACTCATCCGCGCTCCAGAGGCC	1748						
Db	1748	GAGCCCTGCAATGACACCCA-GGCCACCCGCGAGACACTCATCCGCGCTCCAGAGGCC	1795						
QY	1749	CACCCCTCATCAACAGCGCCCGCGAGGAGGGGCTGGGGACTG	1795						
Db	1807	CCACCCCTCAATGCAACAGCCCGGCCCGCAAGGCCAGGGGGCTG	1853						

RESULT 8
US-10-092-900A-55
; Sequence 55, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina

; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Hailong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 55
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(1567)
US-10-092-900A-55

Query Match 73.1%; Score 1601.4; DB 13; Length 1611;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	122	GCSCCAGGTTCCCAACAGGCTACGCAAGAACCCCTTGACTGACCAATGGAGGGG	181
Db	1	GCSCCAGGTTCCCAACAGGCTACGCAAGAACCCCTTGACTGACCAATGGAGGGG	60
QY	182	GGTCCAGCTGTCTGCTGCCAGGATCTCTCGGCGAGAGCTGGTAGAACGGGTGGCAGCCATC	241
Db	61	GGTCCAGCTGTCTGCTGCCAGGATCTCTCGGCGAGAGCTGGTAGAACGGGTGGCAGCCATC	120
QY	242	GATGTGACTCACTTGGAGGAGGAGATGGTGGCCCGACAGCTTACTAGAAACGGTGTGGAC	301
Db	121	GATGTGACTCACTTGGAGGAGGAGATGGTGGCCCGACAGCTTACTAGAAACGGTGTGGAC	180
QY	302	CCCCCACCACGGGCCAGAGCTGCTCTGTGATCTCTGGCGAGTACTTCAAGACTGTCTCCCA	361
Db	181	CCCCCACCACGGGCCAGAGCTGCTCTGTGATCTCTGGCGAGTACTTCAAGACTGTCTCCCA	240
QY	362	GCCCGGCTTAGCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGCAGGAAGCTAT	421
Db	241	GCCCGGCTTAGCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGCAGGAAGCTAT	300
QY	422	CTGAGGCGCAGGCTGGGCTTATAGCCAGGGGCTGCGCAGCCATCTCCCCCGGGGCC	481
Db	301	CTGAGGCGCAGGCTGGGCTTATAGCCAGGGGCTGCGCAGCCATCTCCCCCGGGGCC	360
QY	482	TGGCGAGGCCACCACTCAGTCCACCGTGGCCATCTCAGATCGCAGAGGACTCGGTG	541
Db	361	TGGCGAGGCCACCACTCAGTCCACCGTGGCCATCTCAGATCGCAGAGGACTCGGTG	420

542 CAGCTGAACACAGTACAAAGCTGCAGAGCTGAGATTGGCAAGGGTGCTTACGCTGGTGAGG 601
421 CAGCTGAACACAGTACAAAGCTGCAGAGCTGAGATTGGCAAGGGTGCTTACGCTGGTGAGG 480
602 CTGGCCTTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCTCTTTCCAAAAAGAAG 661
481 CTGGCCTTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCTCTTTCCAAAAAGAAG 540
662 TTACTGAAGCAGTATGGCTTTCCAGTCCGCCCTCCCGAGAGGGTCCAGGTCGCCAG 721
541 TTACTGAAGCAGTATGGCTTTCCAGTCCGCCCTCCCGAGAGGGTCCAGGTCGCCAG 600
722 GGAGGACCAAGCAGAGCTGCTGCCCTCGAGCGGGTGTACCAAGAGATTGGCATCCTG 781
601 GGAGGACCAAGCAGAGCTGCTGCCCTCGAGCGGGTGTACCAAGAGATTGGCATCCTG 660
782 AAGAAGCTCGACCAAGTGAATGTGTCAAACCTGATCGAGTCTCTGATGATCAACCGTGGAG 841
661 AAGAAGCTCGACCAAGTGAATGTGTCAAACCTGATCGAGTCTCTGATGATCAACCGTGGAG 720
842 GACAACTCTATTGTGTGTGACCTCTGAGAAAGGGGCCGTCTATGGAAGTGCCTGT 901
721 GACAACTCTATTGTGTGTGACCTCTGAGAAAGGGGCCGTCTATGGAAGTGCCTGT 780
902 GACAAGCCCTTCTCGAGGAGCAAGCTCGCTCTACTCGGAGACGTCTATCTGGGCGCTC 961
781 GACAAGTCTTCTCGAGGAGCAAGCTCGCTCTACTCGGAGACGTCTATCTGGGCGCTC 840
962 GAGTACTTCTACTGCGAGAGATCGTCCACAGGACATCAAGCCATCAACCTGCTCCTG 1021
841 GAGTACTTCTACTGCGAGAGATCGTCCACAGGACATCAAGCCATCAACCTGCTCCTG 900
1022 GGGGATGATGGGACGTAAGATCGCGACTTGGCGTCAGCAACAGTTTGGGGGGAAC 1081
901 GGGGATGATGGGACGTAAGATCGCGACTTGGCGTCAGCAACAGTTTGGGGGGAAC 960
1082 GACGCTCAGCTGTCCAGCACGCGGGAAACCCAGCAATTTCATGGCCCCCGAGGCGCATTTCT 1141
961 GACGCTCAGCTGTCCAGCACGCGGGAAACCCAGCAATTTCATGGCCCCCGAGGCGCATTTCT 1020
1142 GATTCGCGCAGAGCTTTCAGTGGGAAAGGCTTGGATGTATGGGCCATCTGGCGTCAAGTTG 1201
1021 GATTCGCGCAGAGCTTTCAGTGGGAAAGGCTTGGATGTATGGGCCATCTGGCGTCAAGTTG 1080
1202 TACTGCTTTGTCTATCGGAAGTGCCTCATTCATCGAGATTTCATCTGCGCCCTCCACAGG 1261
1081 TACTGCTTTGTCTATCGGAAGTGCCTCATTCATCGAGATTTCATCTGCGCCCTCCACAGG 1140
1262 AAGATCAAGAATGAGCCCGCTGGTGTTCCTTGAGGAGCCAGAAATCAGCGAGGAGCTCAAG 1321
1141 AAGATCAAGAATGAGCCCGCTGGTGTTCCTTGAGGAGCCAGAAATCAGCGAGGAGCTCAAG 1200
1322 GACCTGATCTGAGATGTAGCAAGAATCCCGAGACAGAAATGGGGTGCAGACATC 1381
1201 GACCTGATCTGAGATGTAGCAAGAATCCCGAGACAGAAATGGGGTGCAGACATC 1260
1382 AAGTTCACCTTGGGTGACCAAGAACGGGGAGGAGCCCTTCTCTTTCGGAGGAGGAGCAC 1441
1261 AAGTTCACCTTGGGTGACCAAGAACGGGGAGGAGCCCTTCTCTTTCGGAGGAGGAGCAC 1320
1442 TGCAAGCTGTGGAGGTGACAGAGGGGGAGGTTTAAAGACTCAGTCAAGGCTCATCTCCCAAG 1501
1321 TGCAAGCTGTGGAGGTGACAGAGGAGGAGGTTTAAAGACTCAGTCAAGGCTCATCTCCCAAG 1380
1502 TGCAACACGGTGTCTGTGAGTCCATGCTGAGGAAGGTTTCTTGGGACCCGTTT 1561
1381 TGCAACACGGTGTCTGTGAGTCCATGCTGAGGAAGGTTTCTTGGGACCCGTTT 1440
1562 GAGCCCCCAGGACCGAGGGAAGAGCGATCCATGCTGTCTCCAGGAAACCTTACTTGTGAAA 1621
1441 GAGCCCCCAGGACCGAGGGAAGAGCGATCCATGCTGTCTCCAGGAAACCTTACTTGTGAAA 1500
1622 GAAGGGTTTGGTGAAGGGGGCAAGAGCCACAGAGCTCCCCGGCGTCCAGGAAGAGGAGCT 1681

Db 1501 GAAGGGTTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGGAAGACGAGGCT 1560
QY 1682 GCATCTGAGCCCTCATGCACCCAGGGGCCACCCGGCAGCAGACATCATCC 1732
Db 1561 GCATCTGAGCCCTCATGCACCCAGGGGCCACCCGGCAGCAGACATCATCC 1611

RESULT 9

US-10-092-900A-53
; Sequence 53, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernov, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Hathong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 53
; LENGTH: 1547
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1529)
US-10-092-900A-53

Query Match 68.2%; Score 1493.8; DB 13; Length 1547;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1530; Conservative 0; Mismatches 17; Indels 6; Gaps 2;
QY 154 AACCCCTTGACTGAAGCAATGAGGGGGTTCAGCTGTCTGTCGACAGATCTCTGGGC 213
Db 1 AACCCCTTGACTGAAGCAATGAGGGGGTTCAGCTGTCTGTCGACAGATCTCTGGGC 60
QY 214 AGAGCTGGTAGAAGCGGTGGCAGCCATCGATGTGACTGTGACTTTGGAGAGGAGAGATGGTGG 273
Db 61 AGAGCTGGTAGAAGCGGTGGCAGCCATCGATGTGACTGTGACTTTGGAGAGGAGAGATGGTGG 120
QY 274 CCCAGAGCCTACTAGAAACGGTGTGGACCCGCCACCCAGCGGGCCAGAGCTGCTCTGTGAT 333
Db 121 CCCAGAGCCTACTAGAAACGGTGTGGACCCGCCACCCAGCGGGCCAGAGCTGCTCTGTGAT 180
QY 334 CCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCTAGCCTCTCAGCCAGGAAGTTTC 393
Db 181 CCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCTAGCCTCTCAGCCAGGAAGTTTC 240
QY 394 CCTACAGGAGCGCCGAGCAGGAAGCTATCTGAGGCGCAGAGGCTGGGCCCTTATGCCACGGG 453
Db 241 CCTACAGGAGCGCCGAGCAGGAAGCTATCTGAGGCGCAGAGGCTGGGCCCTTATGCCACGGG 300
QY 454 GCCTGCCAGCCACATCTCCCGCGGCTGGCGGAGGCCACCATCGAGTCCACACCGT 513
Db 301 GCCTGCCAGCCACATCTCCCGCGGCTGGCGGAGGCCACCATCGAGTCCACACCGT 360
QY 514 GGCATCTCAGATGAGAGGACTGCTGAGCTGAACAGTACAGTACAGTCTCAGAGTGAGAT 573
Db 361 GGCATCTCAGATGAGAGGACTGCTGAGCTGAACAGTACAGTACAGTCTCAGAGTGAGAT 420
QY 574 TGGCAAGGTGCTACGGTGTGGTGGCTGCCTTACAAAGAGTGAAGAGCAGACACTA 633
Db 421 TGGCAAGGTGCTACGGTGTGGTGGCTGCCTTACAAAGAGTGAAGAGCAGACACTA 480
QY 634 TGCATGAAGTCTTTTCCAAAAGAGTTACTGAAGCAGTATGGCTTTCCACGTGCGCC 693
Db 481 TGCATGAAGTCTTTTCCAAAAGAGTTACTGAAGCAGTATGGCTTTCCACGTGCGCC 540
QY 694 TCCCGGAGAGGCTCCAGGCTGCCAGGGAGGACAGCCAGCAGCTGCTGCCCTTGA 753
Db 541 TCCCGGAGAGGCTCCAGGCTGCCAGGGAGGACAGCCAGCAGCTGCTGCCCTTGA 600
QY 754 GCGGTGTACAGGAGATTGCCATCTCAAGAGCTGGACACAGTGAATGTGCTCAAACT 813
Db 601 GCGGTGTACAGGAGATTGCCATCTCAAGAGCTGGACACAGTGAATGTGCTCAAACT 660
QY 814 GATCAGGTCTGGATGACCCAGTGTAGACAACTCTATTGTGGTGTGACCTCTCTGAG 873
Db 661 GATCAGGTCTGGATGACCCAGTGTAGACAACTCTATTGTGGTGTGACCTCTCTGAG 717
QY 874 AAAGGGCCCGCTCATGGAGTGCCTGTGACAGCCCTTCTCGGAGGAGCAGCTCGCT 933
Db 718 CCAAGGCGCGCTCATGGAGTGCCTGTGACAGCCCTTCTCGGAGGAGCAGCTCGCT 777
QY 934 CTACCTCGGGACGTCATCTTGGGGCTCGAGTACTTTCAGTTCGACAGAGATGCTCCACAG 993
Db 778 CTACCTCGGGACGTCATCTTGGGGCTCGAGTACTTTCAGTTCGACAGAGATGCTCCACAG 837
QY 994 GGACATCAAGCCATCCAACTGCTCTGGGGGATGATGGGACAGTGAAGATGCGGACTT 1053
Db 838 GGACATCAAGCCATCCAACTGCTCTGGGGGATGATGGGACAGTGAAGATGCGGACTT 897
QY 1054 TGGCGTCAGCAACCAAGTTTGGAGGGAGCAGCTCAGCTGTCCAGCAGCGGGGAGACCC 1113
Db 898 TGGCGTCAGCAACCAAGTTTGGAGGGAGCAGCTCAGCTGTCCAGCAGCGGGGAGACCC 957

QY	1114	AGCATTTCATGGCCCCCGAGGCCAATTTCTGATTCGGGCCAGAGCTTCAGTGGGAGGCCTT	1173
Db	958	AGCAITTCATGGCCCCCGAGGCCAATTTCTGATTCGGGCCAGAGCTTCAGTGGGAG---	1014
QY	1174	GAATGTATGGGCCCATCGGGGTCA CGTTGTTA CTGCTTTGTTCTATGGGAAGTGCCCATTCAT	1233
Db	1015	GGATGTATGGGCCCATCGGGGTCA CGCTTGTACTGCTTTGTTCTATGGGAAGTGCCCATTCAT	1074
QY	1234	CGACGATTTTCCTCTGGCCCTCCACAGGAAGATCAAGATCAGCCCTGGTGTTCCTGA	1293
Db	1075	CGACGATTTTCCTCTGGCCCTCCACAGGAAGATCAAGATCAGCCCTGGTGTTCCTGA	1134
QY	1294	GGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAAGATGTTAGACAGAATCC	1353
Db	1135	GGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAAGATGTTAGACAGAATCC	1194
QY	1354	CGAGCGAGAAATGGGGTGCAGACATCAAGTTCACCTTGGTGACCAAGAACGGGA	1413
Db	1195	CGAGCGAGAAATGGGGTGCAGACATCAAGTTCACCTTGGTGACCAAGAACGGGA	1254
QY	1414	GGAGGCCCTTCCTTCGGAGGAGGACCTCAGCGGTGGTGGAGGTGACAGAGGGGAGGT	1473
Db	1255	GGAGGCCCTTCCTTCGGAGGAGGACCTCAGCGGTGGTGGAGGTGACAGAGGAGGAGGT	1314
QY	1474	TAAGAACTCAGTCAGGCTCATCCAGCTGAGACCGTGTATCTGTTGAAGTCCATGCT	1533
Db	1315	TAAGAACTCAGTCAGGCTCATCCAGCTGAGACCGTGTATCTGTTGAAGTCCATGCT	1374
QY	1534	GAGGAAGCGTTCCTTTGGGAACCCGTTTGAGCCCCCAGGACCGGAGGGAAGAGCGATCCAT	1593
Db	1375	GAGGAAGCGTTCCTTTGGGAACCCGTTTGAGCCCCCAGGACCGGAGGGAAGAGCGATCCAT	1434
QY	1594	GTCTGCTCCAGGAAACCTACTCGTGAAGAAGGGTTTGGTGAAGGGGCAAGGCCAG	1653
Db	1435	GTCTGCTCCAGGAAACCTACTCGTGAAGAAGGGTTTGGTGAAGGGGCAAGGCCAG	1494
QY	1654	GCTCCCGCGGTCCAGGAAGAGGAGCTGCATCTGAGCCCTGCATCACC	1706
Db	1495	GCTCCCGCGGTCCAGGAAGAGGAGCTGCATCTGAGCCCTGCATCACC	1547
RESULT 10			
US-09-922-138-9			
; Sequence 9, Application US/09922138			
; Patent No. US20020061574A1			
; GENERAL INFORMATION:			
; APPLICANT: Millennium Pharmaceuticals, Inc.			
; APPLICANT: Meyers, Rachel			
; APPLICANT: Silos-Santiago, Immaculada			
; TITLE OF INVENTION: 16658, 14223, AND 16002, NOVEL HUMAN			
; TITLE OF INVENTION: KINASES AND USES THEREFOR			
; FILE REFERENCE: 38155-20030.00			
; CURRENT APPLICATION NUMBER: US/09/922,138			
; PRIOR FILING DATE: 2001-11-28			
; PRIOR APPLICATION NUMBER: US 60/229,299			
; PRIOR FILING DATE: 2000-09-01			
; NUMBER OF SEQ ID NOS: 38			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 9			
; LENGTH: 1683			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-922-138-9			
Query Match 68.1%; Score 1490.6; DB 9; Length 1683;			
Best Local Similarity 99.4%; Pred. No. 0;			
Matches 1496; Conservative 0; Mismatches 9; Indels 0; Gaps 0;			
QY	173	ATGAGGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG	232
Db	1	ATGAGGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG	60

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Db 1141 GAGCTCAAGGACCTGATCTCTGAAGATGTTAGACAAGAAATCCCGAGACGAGAATTGGGGTG 1200
Qy 1373 CCAGACATCAAGTTGCACCTTTGGGTGACCAAGAAACGGGGAGAGCCCTTCTTTCGGAG 1432
Db 1201 CCAGACATCAAGTTGCACCTTTGGGTGACCAAGAAACGGGGAGAGCCCTTCTTTCGGAG 1260
Qy 1433 GAGGAGCATGTCAGCGTGTGTGAGTGAACAGAGGGGGAGGTTAAGAACTCAGTCAGGCTC 1492
Db 1261 GAGGAGCATGTCAGCGTGTGTGAGTGAACAGAGGGGGAGGTTAAGAACTCAGTCAGGCTC 1320
Qy 1493 ATCCCCAGCTGACACAGCGTGTCTCTGGTGAAGTCCATGCTCAGGAAGGTTCTTTGGG 1552
Db 1321 ATCCCCAGCTGACACAGCGTGTCTCTGGTGAAGTCCATGCTCAGGAAGGTTCTTTGGG 1380
Qy 1553 AACCCGTTTGAGCCCCAGGACGAGGAGGAAGCGATCCATGCTCTCCAGGAACCTTA 1612
Db 1381 AACCCGTTTGAGCCCCAGGACGAGGAGGAAGCGATCCATGCTCTCCAGGAACCTTA 1440
Qy 1613 CTGGTGAAGAGGTTTGGTGAAGGGGGCAAGAGCCCGAGAGCTCCCGGCGTCCAGGAA 1672
Db 1441 CTGGTGAAGAGGTTTGGTGAAGGGGGCAAGAGCCCGAGAGCTCCCGGCGTCCAGGCT 1500
Qy 1673 GACGA 1677
Db 1501 TACCA 1505

RESULT 11
US-10-391-364-43
; Sequence 43, Application US/10391364
; Publication No. US20040121349A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Cook, William James
; APPLICANT: Kapeller-libermann, Rosana
; APPLICANT: Weich, Nadine S.
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352,
; TITLE OF INVENTION: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: MP103-0190NM1M
; CURRENT APPLICATION NUMBER: US/10/391,364
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/950,370
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/231,084
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 10/294,039
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/338,587
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 10/266,035
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US 60/328,198
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/717,926
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/214,707
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 10/268,036
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/327,820
; PRIOR FILING DATE: 2001-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1686)
US-10-391-364-43

Query Match 68.1%; Score 1490.6; DB 17; Length 1686;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1496; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 173 ATGAGAGGGGGTCCAGCTGTCTGCTCCAGAGATCCTCGGGCAGAGCTGGTGAACACGGGTG 232
Db 1 ATGAGAGGGGGTCCAGCTGTCTGCTCCAGAGATCCTCGGGCAGAGCTGGTGAACACGGGTG 60
Qy 233 GCAGCCATCGATGTGACTCAGTCTGGAGGAGGAGATGGTGGCCAGAGCCTACTAGAAAC 292
Db 61 GCAGCCATCGATGTGACTCAGTCTGGAGGAGGAGATGGTGGCCAGAGCCTACTAGAAAC 120
Qy 293 GGTGTGGACCCCCACACGCGGCGAGAGTGCTCTGTGATCCCTGGGAGTACTTCAAGA 352
Db 121 GGTGTGGACCCCCACACGCGGCGAGAGTGCTCTGTGATCCCTGGGAGTACTTCAAGA 180
Qy 353 CTGCTCCAGAGCCCGGCTAGCTCTCAGCCAGGAAGCTTTCCTACAGAGAGGGCCAGCA 412
Db 181 CTGCTCCAGAGCCCGGCTAGCTCTCAGCCAGGAAGCTTTCCTACAGAGAGGGCCAGCA 240
Qy 413 GGAAGCTATCTGGAGGCGCAGGCTGGGGCTTTATGCCAGGGGCTTSCCAGGCCACATCTCC 472
Db 241 GGAAGCTATCTGGAGGCGCAGGCTGGGGCTTTATGCCAGGGGCTTSCCAGGCCACATCTCC 300
Qy 473 CCCGGGCTTGGCGGAGGCCACCATCGAGTCCACACAGCTGGGCCATCTCAGATCGAGAG 532
Db 301 CCCGGGCTTGGCGGAGGCCACCATCGAGTCCACACAGCTGGGCCATCTCAGATCGAGAG 360
Qy 533 GACTGCGTGACGTGAACACAGTACAAAGTGCAGAGTGAAGTTGGCAAGGGTGCCTACCGT 592
Db 361 GACTGCGTGACGTGAACACAGTACAAAGTGCAGAGTGAAGTTGGCAAGGGTGCCTACCGT 420
Qy 593 GTGTGAGGCTGGGCTCAACAGAAAGTGAAGACAGACACTATGCAATGAAAGTCTCTTTC 652
Db 421 GTGTGAGGCTGGGCTCAACAGAAAGTGAAGACAGACACTATGCAATGAAAGTCTCTTTC 480
Qy 653 AAAAAGAGTTACTGAGCAGTATGGCTTTCAGTGGCCCTCCCGAGAGGGTCCAG 712
Db 481 AAAAAGAGTTACTGAGCAGTATGGCTTTCAGTGGCCCTCCCGAGAGGGTCCAG 540
Qy 713 GCTGCCAGGAGGACACAGCAGCTGTGCTGCCCTGGAGCGGTGTGTACAGAGAGATT 772
Db 541 GCTGCCAGGAGGACACAGCAGCTGTGCTGCCCTGGAGCGGTGTGTACAGAGAGATT 600
Qy 773 GCCATCCTGAAGAAGCTGGACACAGTGAATGTGGTCAAACTGATCGAGGTCTTGATGAC 832
Db 601 GCCATCCTGAAGAAGCTGGACACAGTGAATGTGGTCAAACTGATCGAGGTCTTGATGAC 660
Qy 833 CCAGCTGAGGACCAACCTTCTATTTGGTGTGACCTCTCGAAGAAAGGGGCCGTCATGAA 892
Db 661 CCAGCTGAGGACCAACCTTCTATTTGGTGTGACCTCTCGAAGAAAGGGGCCGTCATGAA 720
Qy 893 GTGCCCTGTGACAAGCCCTTCTCGAGGAGCAAGCTCGCCCTTACCTGCGGGAGCTCATC 952
Db 721 GTGCCCTGTGACAAGCCCTTCTCGAGGAGCAAGCTCGCCCTTACCTGCGGGAGCTCATC 780
Qy 953 CTGGGCTCTCGAGTACTTGCATGCGCAGAGATCGTCCACAGGGACATCAAGCCATCCAAC 1012
Db 781 CTGGGCTCTCGAGTACTTGCATGCGCAGAGATCGTCCACAGGGACATCAAGCCATCCAAC 840
Qy 1013 CTGCTCTGGGGAGTATGGGCACTGAAGATCGCCGAGCTTTTGGCGTCAGCAACAGTTT 1072
Db 841 CTGCTCTGGGGAGTATGGGCACTGAAGATCGCCGAGCTTTTGGCGTCAGCAACAGTTT 900
Qy 1073 GAGGGGAACGACGCTCAGCTGTCCAGCAGCGGGGAGCCCGAGCATTCATGGCCCCCGAG 1132
Db 901 GAGGGGAACGACGCTCAGCTGTCCAGCAGCGGGGAGCCCGAGCATTCATGGCCCCCGAG 960
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Db 421 CAGCTGAACCAAGTCAAGCTCAGAGTGAGATTGGCAAGGTGCCCTACGGTGTGTGAGG 480
QY 602 TTGGCTTCAACGAAGTGAAGACAGACACTATGCAATGAAAGTCTCTTCCAAAAGAG 661
Db 481 CTGGCTTCAACGAAGTGAAGACAGACACTATGCAATGAAAGTCTCTTCCAAAAGAG 540
QY 662 TTACTGAAGCAGTATGCTTTCCAGTGCCTCTCCCGAGAGGGTCCAGAGTGCCTG 721
Db 541 TTACTGAAGCAGTATGCTTTCCAGTGCCTCTCCCGAGAGGGTCCAGAGTGCCTG 600
QY 722 GGAGACCAAGCAAGCAGTGTGCTGCTCCCTGGAGCGGTGTACAGAGATTGCCATCTG 781
Db 601 GGAGACCAAGCAAGCAGTGTGCTGCTCCCTGGAGCGGTGTACAGAGATTGCCATCTG 660
QY 782 AAGAGCTGGACCAAGTGAATGTGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGAG 841
Db 661 AAGAGCTGGACCAAGTGAATGTGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGAG 720
QY 842 GACACCTCTATTG----- 856
Db 721 GACACCTCTATTG----- 856
QY 857 ----- 856
Db 781 ATCGCAAGTCCACTCCCTGCTTCCCTCTGAGCAGCAAGCAGTGGATCCAGTGGGCT 840
QY 857 -----GTGTTGACTCTCTGAGAAAGGGCCCGTCAATGGAAGTGCCTGTGACAAAG 907
Db 841 GCGCGCTCAGTGTGTTGACTCTCTGAGAAAGGGCCCGTCAATGGAAGTGCCTGTGACAAAG 900
QY 908 CCTTCTCGAGGACCAAGCTGCCTCTACCTCGGGAGCGTCACTCGGGCTCAGTAC 967
Db 901 CCTTCTCGAGGACCAAGCTGCCTCTACCTCGGGAGCGTCACTCGGGCTCAGTAC 960
QY 968 TTCACTCCGAGAGATCGTCCACAGGACATCAAGCCATCAACCTGCTCTGGGGAT 1027
Db 961 TTCACTCCGAGAGATCGTCCACAGGACATCAAGCCATCAACCTGCTCTGGGGAT 1020
QY 1028 GATGGGCAAGTGAAGTCCCGACTTTGGCGTCAGCAACCAAGTGTGAGGGGAACGACGT 1087
Db 1021 GATGGGCAAGTGAAGTCCCGACTTTGGCGTCAGCAACCAAGTGTGAGGGGAACGACGT 1080
QY 1088 CAGCTGTCCAGCAGCGCGGACCCAGCATTCATGGCCCGGAGGCCATTTCTGATTC 1147
Db 1081 CAGCTGTCCAGCAGCGCGGAAACCCAGCATTCATGGCCCGGAGGCCATTTCTGATTC 1140
QY 1148 GCGCAGAGCTTCAGTGGGAAGGCTTTGGATGATGGGCCACTGGCGTCACGTTGACTGC 1207
Db 1141 GCGCAGAGCTTCAGTGGGAAGGCTTTGGATGATGGGCCACTGGCGTCACGTTGACTGC 1200
QY 1208 TTTGTTATGGGAAGTGCCTCAATTCAGCAATTTTCATCTGGCCCTCCACAGGAAGATC 1267
Db 1201 TTTGTTATGGGAAGTGCCTCAATTCAGCAATTTTCATCTGGCCCTCCACAGGAAGATC 1260
QY 1268 AAGATGAGCGCTGCTGTTCTCAGGAGCGCAGAAATCAGCGAGAGCTCAAGACCTG 1327
Db 1261 AAGATGAGCGCTGCTGTTCTCAGGAGCGCAGAAATCAGCGAGAGCTCAAGACCTG 1320
QY 1328 ATCTCTGAAGATGTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTG 1387
Db 1321 ATCTCTGAAGATGTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTG 1380
QY 1388 CACCTTGGGTGACCAAGAACGGGAGAGGAGCCCTTCTCTGGAGGAGGACCTGCGAC 1447
Db 1381 CACCTTGGGTGACCAAGAACGGGAGAGGAGCCCTTCTCTGGAGGAGGACCTGCGAC 1440
QY 1448 GTGTGGAGGTCACAGAGGGGAGGTTAAGAACTCAGTCAAGCTCATCCAGCTGGACC 1507
Db 1441 GTGTGGAGGTCACAGAGGGGAGGTTAAGAACTCAGTCAAGCTCATCCAGCTGGACC 1500
QY 1508 ACGGTGATCTCGTGAAGTGCATGTGAGGAAGCGTTCCTTTGGAAACCGCTTTGAGGCC 1567
Db 1501 ACGGTGATCTCGTGAAGTGCATGTGAGGAAGCGTTCCTTTGGAAACCGCTTTGAGGCC 1560

RESULT 13

US-10-295-027-1138
; Sequence 1138, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glyme, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1138
; LENGTH: 5611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1138

Query Match 29.8%; Score 653.6; DB 16; Length 5611;
Best Local Similarity 70.7%; Pred. No. 2.2e-169;

Matches 899; Conservative 0; Mismatches 369; Indels 4; Gaps 2;

QY 439 GCCTTATGCCACGGGGCTGCAGCCACATCTCCCCCGGGCCCTGGCGGAGGCCCAT 498
Db 1201 GCCCTACTCACCCGTCAGTCCCGCAGTCTCGCTCGGCTGCCCGGGCGGACAGT 1260
QY 499 CGAGTCCACACGCTGGCCATCTCAGATGCAGAGAGCTGCGTGCAGTGAACAGTACAA 558

Db 1261 GGGTCTCACCAGCTCTCCATCAGGGGTATGAGGACTGTGTGACGTGAATCAGTATAC 1320
Qy 559 GCTGCAAGTGAATGGCAAGGTGCCTACGGTGTGGTGAAGCTGCGCTTACCAACGAAG 618
Db 1321 CCTGAAGTGAATTTGGAAGGGCTCTATGGTGTGCTCAAGTTGGCTTACATGAAA 1380
Qy 619 TGAAGCAGACATATGACATGAAGTCTTTCCAAAGAAAGTTACTGAAGCAGTATGG 678
Db 1381 TGACATACCTACTATGCAATGAAGTGTGTCCAAAAGAAAGTCAATCCGGAGCGCG 1440
Qy 679 CTTTCCACGTGCGCTCCCCGAGAGGGTCCAGGCTGCCAGGGAGCAACAGCAAGCA 738
Db 1441 CTTTCCACGTGCGCTCCACCCGAGGACCCGCGCAGCTCTCTGGAGCTGCATCCAGC 1500
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Qy 799 GAATGTGTCACAACTGATCAGGTCTCTGGATGACCCAGCTGAGACAACTCTATTGGT 858
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Qy 859 GTTTGACCTCTCAGAAAGGGCGCGCTCATGGAAGTCCCTGTGCAAGGCCCTTCTCGGA 918
Db 1621 GTTCGAATGTCACCAAGGGCCGCTGATGGAAGTCCCACTCAACCACTCTCTGA 1680
Qy 919 GAGCAAGCTGCGCTTACTCTGGGGAGCTATCTCTGGGCTCGAGTACTGACTGCCA 978
Db 1681 AGACCAAGCGCGTTTCTACTTCCAGGATCTGATCAAGGATCGAGTACTTACACTCA 1740
Qy 979 GAAGATCGTCCAGGACACATCAAGCCATCAACCTGCTCTGGGGATGATGGCAGT 1038
Db 1741 GAAGATCAATCACCGTGACATCAACCTTCAACCTCTGTCGGAGAGATGGGACAT 1800
Qy 1039 GAAGATCGCGACTTTGGCGCTCAGCAACCACTGTTGAGGGAAACAGCCTCAGCTGTCCAG 1098
Db 1801 CAAGATCGCTGACTTTGGTGTGAGCAATGAATCAAGGGCAGTACGCGCTCTCTCAA 1860
Qy 1099 CAGGGGGAAACCCAGCATTCATGGCCCGGAGGCCATTTCTGATTCGGCCAGAGCTT 1158
Db 1861 CACCGTGGGACGCGCCCTTCATGGCACCGGAGTCTCTCTGAGACCCGCAAGATCTT 1920
Qy 1159 CAGTGGAAAGCCTTTGATGTATGGGCACTGGGCTCAGCTTGCTGCTTTGCTATGG 1218
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Qy 1219 GAAGTGCCCAATTCATGACGATTTTCATCTGGGCCCTCCACAGGAAGATCAAGATGACC 1278
Db 1981 CCAAGTGCCCAATTCATGACGAGCGGATCATGTGTTTACAGATCAAGATCAAGCTCAGGC 2040
Qy 1279 CGTGGTGTCTTCTGAGGAGCAGAAATCAGGAGGAGCTCAGGACCTGATCTCTGAGAT 1338
Db 2041 CTTGGAAATTTCCAGACCGCCGACATAGCTGAGGACTTGAAGGACCTGATCAACCCGTAT 2100
Qy 1339 GTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTGACCCCTGGGT 1398
Db 2101 GCTGGACAGAAACCCCGAGTCAGATGCTGGTGTCCGGAATCAAGCTGACCCCTGGT 2160
Qy 1399 GACCAAGAACGGGAGGAGGCCCTTCTTCTGGAGGAGGACATGTCAGCGTGTGGAGGT 1458
Db 2161 CACGAGGATGGGGCGGAGCGTTTGGCGTGGAGGATGAGAACTGACGCTGTGCGAAT 2220
Qy 1459 GACAGGGGGAGGTGAAGACTCAGTCAGCTCATCCAGCTGACACCGGATGATCCT 1518
Db 2221 GACTGAAGAGAGGTGAGAACTCAGTCAACACATTTCCAGCTTGGCAACCGGATCTCT 2280
Qy 1519 GGTGAAGTCCATGCTGAGGAAGCCTTCTTTGGGAACCCGTTTGGAGCCCGCAGGACGGAG 1578
Db 2281 GGTGAAGACCATGATACGTAACGCTCTTTGGGAACCCCATTCAGGGGC---AGCCGGCG 2337
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RESULT 14

US-10-316-124-7
; Sequence 7, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: MPI01-291PIRM
; CURRENT APPLICATION NUMBER: US/10/316,124
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4427
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-316-124-7

Query Match 29.7%; Score 651.2; DB 15; Length 4427;

Best Local Similarity 71.3%; Pred. No. 9.5e-169;

Matches 873; Conservative 0; Mismatches 348; Indels 3; Gaps 1;

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Db 360 GCCTTACTACCGCTCAGCTCCCGCAGTCTCTGCTCGCTCGCTGCCCGCGCGGACAGT 419
Qy 499 CGAGTCCCACCAAGTGGCCATCTCAGATGAGAGGAGTGTGTCAGTGAACAGTACAA 558
Db 420 GGAGTCTCACCGCTCTCCATCACGGGTATGCGAGGAGTGTGTCAGTGAATCAGTATAC 479
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Db 480 CCTGAAGATGAATTTGAAAGGGCTCCTATGGTGTGCTCAGTTGGCTTACATGAAA 539
Qy 619 TGAAGACAGACACTATGCAATGAAAGTCTTTTCCAAAAAGAGTTACTGAAGCAGTATGG 678
Db 540 TGACATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAGTGTATCGGAGGCGCG 599
Qy 679 CTTTCCAGTCTGCGCTTCCCCGAGAGGCTCCGAGGCTGCCAGGAGGACGAGCCAGCA 738
Db 600 CTTTCCAGTCTGCGCTTCCACCCGAGGACCCCGCCAGCTCCTGGAGGCTGCAATCCAGCC 659
Qy 739 GCTGCTGCCCTGGAGCGGTGTACAGGAGATTGCCATCCTGAAGAGTGTGACCAAGT 798
Db 660 CAGGGCCCCCTTGAAGAGGTCACAGGAAATTTGCCATCTCTCAAGAGTGTGACCAACC 719
Qy 799 GAATGTGTCACAACTGATCGAGGTCTCTGGATGACCCAGCTGAGGACAACTCTATTGGT 858
Db 720 CAATGTGTTGAAGTGTGTGGAGTCTCTGGATGACCCCAATGAGACCATCTGTACATGGT 779
Qy 859 GTTTGACCTCTGAGAAAGGGCCGCTCATGGAAGTGCCTGTGACAGGCCCTTCTCGGA 918
Db 780 GTTCGAATCGTCAACCAAGGGCCCGGTGATGGAAGTGCCTCCCTCAACCACTCTCTGA 839
Qy 919 GGAAGCAAGCTCGCTCTTACCTGCGGAGCTCATCTCTGGGCTCGAGTACTTTGCACTGCCA 978
Db 840 AGACCAAGCGCGTTTCTTACTTCCAGGATCTGATCAAGAGGATCGAGTACTTACACTACCA 899
Qy 979 GAAGATCGTCCACAGGAGACATCAAGCCATCAACCTGCTCTCTGGGGGATGATGGGCAAGT 1038

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QY 1039 GAAGATCGCCGACTTTGGCGTCAGCAACAGATTTGAGGGGAACGACGCTCAGCTGTCCAG 1098
Db 960 CAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAGGGCAGTGACGCGCTCTCTCCAA 1019
QY 1099 CACGGCGGGAACCCAGCAATTCATGGCCCCCGAGGCGCATTTCTGATTCGGGCAAGGTTT 1158
Db 1020 CACCGTGGGCAACCGCGCGCTTCATGGCACCCGAGTGTCTCTGAGACCCGCAAGATCTT 1079
QY 1159 CAGTGGGAAGCGCTTGGATGATGGGCACTCGCGCTCAGCTGTGATCTGCTTGTCTATGG 1218
Db 1080 CTCGGGAAGCGCTTGGATGATGGGCACTCGCGCTCAGCTGTGATCTGCTTGTCTTGG 1139
QY 1219 GAAGTGCCCATTCATCGACGATTTTCATCTCGCCCTCCACAGGAAGATCAAGAAATGAGCC 1278
Db 1140 CAGTGCCCATTCATCGACGCGGATCATGTGTTTACACAGTAAGATCAAGATCAGGC 1199
QY 1279 CGTGTGTTTCTGAGGAGCCAGAAATCAGCGAGGCTCAAGGACCTGATCTCTGAAAGAT 1338
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US-10-316-124-8
; Sequence 8, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyeung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: MP101-291PIRM
; CURRENT APPLICATION NUMBER: US/10/316,124
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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US-10-316-124-8
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Query Match 29.7%; Score 651.2; DB 15; Length 4427;
Best Local Similarity 71.3%; Pred. No. 9.5e-169;
Matches 873; Conservative 0; Mismatches 348; Indels 3; Gaps 1;

QY 439 GCCTTATGCCAGGGGCGCTGCGCAGCACAATCTCCCGCGGGCTGGCGAGGCGCCACCAT 498
Db 360 GCGCTACTACTACCCGTCAGCTCCCGCAGTCTCTCGCTCGGCTGCGCGCGCGCGCCAGCAT 419
QY 499 CAGTCCCAACACGCTGGCCATCTCAGATGCGAGGACTGCGTGCGAGCTGAACACGATACAA 558
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QY	1579	GGAAAGCGATCCATGCTCTCTCCAGGAACCTACTGTTGAAAGAGGGTTTGGTGAAGG	1638
Db	1497	GGAGGAACGCTCACTGTACGGCTCGAAACTTGTCTCACCACCAAAACCAACCGGGAATG	1556
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Db	1557	TGAGTCCCTGTCTGAGCTCAAGG	1580

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 Job time : 1383 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 04:53:05 ; Search time 1695 Seconds
(without alignments)
92.931 Million cell updates/sec

Title: US-10-690-617-2

Perfect score: 2634

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 31191243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2634	100.0	505	13	US-10-135-689-2
2	2634	100.0	505	16	US-10-690-617-2
3	2626	99.7	505	12	US-10-333-314-19
4	2611	99.1	505	12	US-10-092-900A-56
5	2595	98.5	513	12	US-10-168-582-2
6	2591	98.4	561	9	US-09-922-138-8
7	2591	98.4	561	16	US-10-391-364-42
8	2585	98.1	543	12	US-10-092-900A-58
9	2560	97.2	503	12	US-10-092-900A-54
10	2468	93.7	505	13	US-10-135-689-4
11	2468	93.7	505	16	US-10-690-617-4
12	1525.5	57.9	566	14	US-10-205-823-52
13	1518.5	57.6	588	14	US-10-316-124-9
14	1518.5	57.6	588	15	US-10-295-027-1355
15	1472.5	55.9	417	14	US-10-205-823-54

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16 1043 39.6 357 15 US-10-369-493-5728 Sequence 5728, Ap
17 923 35.0 210 12 US-10-296-115-759 Sequence 759, App
18 649.5 24.7 465 15 US-10-369-493-3141 Sequence 3141, Ap
19 620 23.5 652 16 US-10-618-581-28 Sequence 28, Appl
20 611 23.2 140 12 US-10-296-115-986 Sequence 986, App
21 566 21.5 1142 15 US-10-369-493-1767 Sequence 1767, Ap
22 546.5 20.7 426 12 US-10-618-581-26 Sequence 26, Appl
23 546.5 20.7 426 12 US-10-425-114-50357 Sequence 50357, A
24 541.5 20.6 332 12 US-10-425-114-71396 Sequence 71396, A
25 535 20.3 256 12 US-09-964-956-72 Sequence 72, Appl
26 535 20.3 256 12 US-10-042-865-83 Sequence 83, Appl
27 535 20.3 256 12 US-10-029-020-183 Sequence 183, App
28 535 20.3 256 12 US-10-072-012-799 Sequence 799, App
29 535 20.3 256 12 US-10-072-012-856 Sequence 856, App
30 535 20.3 256 12 US-10-072-012-876 Sequence 876, App
31 535 20.3 256 12 US-10-072-012-882 Sequence 882, App
32 535 20.3 256 16 US-10-055-569A-99 Sequence 99, Appl
33 534 20.3 254 15 US-10-074-978A-150 Sequence 150, App
34 534 20.3 256 10 US-09-863-776-40 Sequence 40, Appl
35 528 20.0 255 12 US-10-087-684-98 Sequence 98, Appl
36 528 20.0 255 12 US-10-218-779-98 Sequence 98, Appl
37 527.5 20.0 426 16 US-10-437-963-162422 Sequence 162422,
38 527 20.0 251 15 US-10-052-648A-41 Sequence 41, Appl
39 526 20.0 250 10 US-09-976-782-31 Sequence 31, Appl
40 526 20.0 252 15 US-10-074-978A-160 Sequence 160, App
41 519 19.7 250 12 US-10-042-865-102 Sequence 102, App
42 518.5 19.3 1408 16 US-10-618-581-29 Sequence 29, Appl
43 507.5 19.7 560 15 US-10-369-493-21916 Sequence 21916, A
44 504 19.1 256 10 US-09-823-187-96 Sequence 96, Appl
45 496 18.8 234 15 US-10-231-913-266 Sequence 266, App

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ALIGNMENTS

RESULT 1

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US-10-135-689-2
; Sequence 2, Application US/10135689
; Publication No. US20020123121A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00904DIV
; CURRENT APPLICATION NUMBER: US/10/135,689
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-689-2

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Query Match 100.0%; Score 2634; DB 13; Length 505;
Best Local Similarity 100.0%; Pred. No. 5.4e-205;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 LLPARPSLSARKLSQERPAAGSYLEAQAQPVATGPASHISPRAWRRTTISHHVAISDAE 120
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QY 481 LVKEGFGGKSPELPGVQDEAAS 505
Db 481 LVKEGFGGKSPELPGVQDEAAS 505
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; Sequence 2, Application US/10690617
; Publication No. US20040086926A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904DIV II
; CURRENT APPLICATION NUMBER: US/10/690,617
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-690-617-2
Query Match 100.0%; Score 2634; DB 16; Length 505;
Best Local Similarity 100.0%; Pred. No. 5.4e-205;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGGPVCCQDPRAELVERVAADIVTHLEADGGPEPTRNGVDPPEPRARAASVIPGSTSR 60
Db 1 MEGGPVCCQDPRAELVERVAADIVTHLEADGGPEPTRNGVDPPEPRARAASVIPGSTSR 60
QY 61 LLPARPSLSARKLSLOERPAGSYLEAQAQPYATGPASHISPAWRRTTIESHHVAISDAE 120
Db 61 LLPARPSLSARKLSLOERPAGSYLEAQAQPYATGPASHISPAWRRTTIESHHVAISDAE 120
QY 121 DCVQLNQYKLSQEIHGKAGVVRVLAAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSQ 180
Db 121 DCVQLNQYKLSQEIHGKAGVVRVLAAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSQ 180
QY 181 AAQGGPAKQLPLERVYQEIALLKLDHNVVVKLIIEVLDDPAEDNLYLVFDLLRKGPVME 240
Db 181 AAQGGPAKQLPLERVYQEIALLKLDHNVVVKLIIEVLDDPAEDNLYLVFDLLRKGPVME 240
QY 241 VPCDKPFSBEOARLYLRDVLGLGLEYLHCQKIVHRDIKPSNLLGGDGHVKIADFGVSNQF 300

Db 241 VPCDKPFSBEOARLYLRDVLGLGLEYLHCQKIVHRDIKPSNLLGGDGHVKIADFGVSNQF 300
QY 301 EGNDAQLSSTAGTAPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFYVYKCPFIIDDFILA 360
Db 301 EGNDAQLSSTAGTAPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFYVYKCPFIIDDFILA 360
QY 361 LHRKIKNEPVVFPPEPPISEELKDLILKMLDKNPETRIGVDPDIKLPWVTNKGEEPLPSE 420
Db 361 LHRKIKNEPVVFPPEPPISEELKDLILKMLDKNPETRIGVDPDIKLPWVTNKGEEPLPSE 420
QY 421 EHCSCVVVEVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARRERSMSAPGNL 480
Db 421 EHCSCVVVEVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARRERSMSAPGNL 480
QY 481 LVKEGFGGKSPELPGVQDEAAS 505
Db 481 LVKEGFGGKSPELPGVQDEAAS 505
RESULT 3
US-10-333-314-19
; Sequence 19, Application US/10333314
; Publication No. US20030211093A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
; APPLICANT: HAPALIA, April J. A.; CHAWLA, Navinder K.
; APPLICANT: ARVIZO, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: GANDHI, Aneena R.; POLICKY, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.
; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAL, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: FI-0162 USN
; CURRENT APPLICATION NUMBER: US/10/333,314
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: PCT/US01/23092
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,038
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/222,112
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,831
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,729
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2190612CD1
US-10-333-314-19
Query Match 99.7%; Score 2626; DB 12; Length 505;
Best Local Similarity 99.8%; Pred. No. 2.4e-204;
Matches 504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MEGGPVCCQDPRAELVERVAADIVTHLEADGGPEPTRNGVDPPEPRARAASVIPGSTSR 60
Db 1 MEGGPVCCQDPRAELVERVAADIVTHLEADGGPEPTRNGVDPPEPRARAASVIPGSTSR 60

QY 61 LLPARPSLSARKLSLOERPAGSYLEAQAQGYATGPASHISPRAWRPTTIESHHVAISDAE 120
DB 61 LLPARPSLSARKLSLOERPAGSYLEAQAQGYATGPASHISPRAWRPTTIESHHVAISDAE 120
QY 121 DCVOLNOYKLOSEIGKAGYGVVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRRPPRGSO 180
DB 121 DCVOLNOYKLOSEIGKAGYGVVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRRPPRGSO 180
QY 181 AAQGGPAKQLPLERVYQEIALLKLDHVNVLKLEVLDDPAEDNLVLFVDFLLRKGPMVE 240
DB 181 AAQGGPAKQLPLERVYQEIALLKLDHVNVLKLEVLDDPAEDNLVLFVDFLLRKGPMVE 240
QY 241 VPCDKPFSSEQARLYLRDVLGLYHLCQKIVHRDIKPSNLLDGGDGHVKIADFGVSNQF 300
DB 241 VPCDKPFSSEQARLYLRDVLGLYHLCQKIVHRDIKPSNLLDGGDGHVKIADFGVSNQF 300
QY 301 EGNDAQLSSTAGTPAPMAPEALSDSGSFGKALDVMATGVTLYCFVYKCPFIIDFFILA 360
DB 301 EGNDAQLSSTAGTPAPMAPEALSDSGSFGKALDVMATGVTLYCFVYKCPFIIDFFILA 360
QY 361 LHRKIKNEPVVPEPEISEELKDLILKMLDKNPETRIGVDPDIKLPWYTKNGEPLPSE 420
DB 361 LHRKIKNEPVVPEPEISEELKDLILKMLDKNPETRIGVDPDIKLPWYTKNGEPLPSE 420
QY 421 EHCSSVVEVTEEVKNVSLIPSWTTLVVKMLKRSFGNPFEPQARREERSMAGPGL 480
DB 421 EHCSSVVEVTEEVKNVSLIPSWTTLVVKMLKRSFGNPFEPQARREERSMAGPGL 480
QY 481 LVKEGFGEGGKSPELPGVQDEAAS 505
DB 481 LVKEGFGEGGKSPELPGVQDEAAS 505

RESULT 4

US-10-092-900A-56
; Sequence 56, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sashu
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092, 900A
; CURRENT FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 56
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-56

Query Match 99.1%; Score 2611; DB 12; Length 505;
Best Local Similarity 99.4%; Pred. No. 4e-203;
Matches 502; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPAPPRARAASVIGSTSR 60
DB 1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPAPPRARAASVIGSTSR 60
QY 61 LLPARPSLSARKLSLOERPAGSYLEAQAQGYATGPASHISPRAWRPTTIESHHVAISDAE 120
DB 61 LLPARPSLSARKLSLOERPAGSYLEAQAQGYATGPASHISPRAWRPTTIESHHVAISDAE 120
QY 121 DCVOLNOYKLOSEIGKAGYGVVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRRPPRGSO 180
DB 121 DCVOLNOYKLOSEIGKAGYGVVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRRPPRGSO 180
QY 181 AAQGGPAKQLPLERVYQEIALLKLDHVNVLKLEVLDDPAEDNLVLFVDFLLRKGPMVE 240
DB 181 AAQGGPAKQLPLERVYQEIALLKLDHVNVLKLEVLDDPAEDNLVLFVDFLLRKGPMVE 240
QY 241 VPCDKPFSSEQARLYLRDVLGLYHLCQKIVHRDIKPSNLLDGGDGHVKIADFGVSNQF 300
DB 241 VPCDKPFSSEQARLYLRDVLGLYHLCQKIVHRDIKPSNLLDGGDGHVKIADFGVSNQF 300
QY 301 EGNDAQLSSTAGTPAPMAPEALSDSGSFGKALDVMATGVTLYCFVYKCPFIIDFFILA 360
DB 301 EGNDAQLSSTAGTPAPMAPEALSDSGSFGKALDVMATGVTLYCFVYKCPFIIDFFILA 360
QY 361 LHRKIKNEPVVPEPEISEELKDLILKMLDKNPETRIGVDPDIKLPWYTKNGEPLPSE 420
DB 361 LHRKIKNEPVVPEPEISEELKDLILKMLDKNPETRIGVDPDIKLPWYTKNGEPLPSE 420
QY 421 EHCSSVVEVTEEVKNVSLIPSWTTLVVKMLKRSFGNPFEPQARREERSMAGPGL 480
DB 421 EHCSSVVEVTEEVKNVSLIPSWTTLVVKMLKRSFGNPFEPQARREERSMAGPGL 480
QY 481 LVKEGFGEGGKSPELPGVQDEAAS 505
DB 481 LVKEGFGEGGKSPELPGVQDEAAS 505

RESULT 5

US-10-168-582-2
; Sequence 2, Application US/10168582
; Publication No. US20040058426A1

```
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Juming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/168,582
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058426A1 2041716CD1
US-10-168-582-2

Query Match      98.5%; Score 2595; DB 12; Length 513;
Best Local Similarity 97.9%; Pred. No. 8.1e-202;
Matches 503; Conservative 0; Mismatches 1; Indels 10; Gaps 2;

Qy      1 MEGGPAVCCDDPRAELVERVAADVTTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
Db      1 MEGGPAVCCDDPRAELVERVAADVTTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60

Qy      61 LLPARPSLSARKLSLOERPAGSYLEAQAQPYATGPASHISPRAWRRPTTIESHHVAISDAE 120
Db      61 LLPARPSLSARKLSLOERPAGSYLEAQAQPYATGPASHISPRAWRRPTTIESHHVAISDAE 120

Qy      121 DCVQLNQYKLOSETGK-----GAYGVVRLAYNESDRHYAMKVLKSKLLKQYGF 171
Db      121 DCVQLNQYKLOSETGKGLTDAIYQAGYGVVRLAYNESDRHYAMKVLKSKLLKQYGF 180

Qy      172 RPPPPGSAQAQGPAPKQLPLERVYQEIALLKLDHVNVLKLEVLDDPAEDNLVLF 231
Db      181 RPPPPGSAQAQGPAPKQLPLERVYQEIALLKLDHVNVLKLEVLDDPAEDNLVLF-D 239

Qy      232 LLRKGPMVEPCDKPFSEEQARLYLDRVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKI 291
Db      240 LLRKGPMVEPCDKPFSEEQARLYLDRVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKI 299

Qy      292 ADFGVSQNFEGNDAQLSSTAGTAPFAPEAISDSQSGSKALDVWATGVTLYCFVYGK 351
Db      300 ADFGVSQNFEGNDAQLSSTAGTAPFAPEAISDSQSGSKALDVWATGVTLYCFVYGK 359

Qy      352 PFIDDFILALHRTIKNEPVFPPEPEISEELKDLILKMLDKNPETRGVDDIKLHPWTK 411
Db      360 PFIDDFILALHRTIKNEPVFPPEPEISEELKDLILKMLDKNPETRGVDDIKLHPWTK 419

Qy      412 NGEPLPSEEHCSVWVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARRE 471
Db      420 NGEPLPSEEHCSVWVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARRE 479

Qy      472 RMSAPGNLLVKEGFGGKSPPLPGVQDEAAS 505
Db      480 RMSAPGNLLVKEGFGGKSPPLPGVQDEAAS 513

RESULT 6
US-09-922-138-8
; Sequence 8, Application US/09922138
```

```
; Patent No. US20020061574A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 1658, 1423, AND 16002, NOVEL HUMAN
; TITLE OF INVENTION: KINASES AND USES THEREFOR
; FILE REFERENCE: 38155-20030.00
; CURRENT APPLICATION NUMBER: US/09/922,138
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/229,299
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-138-8

Query Match      98.4%; Score 2591; DB 9; Length 561;
Best Local Similarity 99.6%; Pred. No. 1.9e-201;
Matches 497; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MEGGPAVCCDDPRAELVERVAADVTTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
Db      1 MEGGPAVCCDDPRAELVERVAADVTTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60

Qy      61 LLPARPSLSARKLSLOERPAGSYLEAQAQPYATGPASHISPRAWRRPTTIESHHVAISDAE 120
Db      61 LLPARPSLSARKLSLOERPAGSYLEAQAQPYATGPASHISPRAWRRPTTIESHHVAISDAE 120

Qy      121 DCVQLNQYKLOSETGKAGYGVVRLAYNESDRHYAMKVLKSKLLKQYGP 180
Db      121 DCVQLNQYKLOSETGKAGYGVVRLAYNESDRHYAMKVLKSKLLKQYGP 180

Qy      181 AAGGPAKQLPLERVYQEIALLKLDHVNVLKLEVLDDPAEDNLVLF 240
Db      181 AAGGPAKQLPLERVYQEIALLKLDHVNVLKLEVLDDPAEDNLVLF 240

Qy      241 VPCDKPFSEEQARLYLDRVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300
Db      241 VPCDKPFSEEQARLYLDRVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300

Qy      301 EGNDAQLSSTAGTAPFAPEAISDSQSGSKALDVWATGVTLYCFVYKCPFI 360
Db      301 EGNDAQLSSTAGTAPFAPEAISDSQSGSKALDVWATGVTLYCFVYKCPFI 360

Qy      361 LHRKIKNEPVFPPEPEISEELKDLILKMLDKNPETRGVDDIKLHPWTKNGEPLPSE 420
Db      361 LHRKIKNEPVFPPEPEISEELKDLILKMLDKNPETRGVDDIKLHPWTKNGEPLPSE 420

Qy      421 EHCSSVVEVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARREERSAPGNL 480
Db      421 EHCSSVVEVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARREERSAPGNL 480

Qy      481 LVKEGFGGKSPPLPGVQ 499
Db      481 LVKEGFGGKSPPLPGVQ 499

RESULT 7
US-10-391-364-42
; Sequence 42, Application US/10391364
; Publication No. US20040121349A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Cook, William James
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Weich, Nadine S.
; APPLICANT: Bandaru, Rajasekhar
```

1 TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352,
2 TITLE OF INVENTION: 16558 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND
3 TITLE OF INVENTION: US95 THEREFOR
4 FILE REFERENCE: MPI03-0190NMIM
5 CURRENT APPLICATION NUMBER: US/10/391,364
6 CURRENT FILING DATE: 2003-03-18
7 PRIOR FILING DATE: US 09/950,370
8 PRIOR FILING DATE: 2001-09-10
9 PRIOR APPLICATION NUMBER: US 60/231,084
10 PRIOR FILING DATE: 2000-09-08
11 PRIOR APPLICATION NUMBER: US 10/294,039
12 PRIOR FILING DATE: 2002-11-13
13 PRIOR APPLICATION NUMBER: US 60/338,587
14 PRIOR FILING DATE: 2001-11-13
15 PRIOR APPLICATION NUMBER: US 10/266,035
16 PRIOR FILING DATE: 2002-10-07
17 PRIOR APPLICATION NUMBER: US 60/328,198
18 PRIOR FILING DATE: 2001-10-09
19 PRIOR APPLICATION NUMBER: US 09/717,926
20 PRIOR FILING DATE: 2000-11-21
21 PRIOR APPLICATION NUMBER: US 60/214,707
22 PRIOR FILING DATE: 2000-06-27
23 PRIOR APPLICATION NUMBER: US 10/268,036
24 PRIOR FILING DATE: 2002-10-09
25 PRIOR APPLICATION NUMBER: US 60/327,820
26 PRIOR FILING DATE: 2001-10-09
27 Remaining Prior Application data removed - See File Wrapper or PALM.
28 NUMBER OF SEQ ID NOS: 93
29 SOFTWARE: FastSeq for Windows Version 4.0
30 SEQ ID NO 42
31 LENGTH: 561
32 TYPE: PRT
33 ORGANISM: Homo sapiens
34 US-10-391-364-42

Query Match 98.4%; Score 2591; DB 16; Length 561;
Best Local Similarity 99.6%; Pred. No. 1.9e-201;
Matches 497; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MEGGPAVCCDPAELVERVAIDVTHLEADGGPEPTRNGVDPPPRAAASVIFGSTR 60
DB 1 MEGGPAVCCDPAELVERVAIDVTHLEADGGPEPTRNGVDPPPRAAASVIFGSTR 60
QY 61 LPARPSLSARKLSQERPAQGYATGASHISPAWRPTIESHHVAISDAE 120
DB 61 LPARPSLSARKLSQERPAQGYATGASHISPAWRPTIESHHVAISDAE 120
QY 121 DCVQLNQYKLOEIGKYGAVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSQ 180
DB 121 DCVQLNQYKLOEIGKYGAVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSQ 180
QY 181 AAQGPAPKQLPLERYQEIALLKLDHVNKKLIEVLDPAEDNLVFDLLRKGPMVE 240
DB 181 AAQGPAPKQLPLERYQEIALLKLDHVNKKLIEVLDPAEDNLVFDLLRKGPMVE 240
QY 241 VPCDKPFSEEARLYRDLVILGLEVHCQKIVHRDIPKSNLLGDDGHVKIADFGVSNQF 300
DB 241 VPCDKPFSEEARLYRDLVILGLEVHCQKIVHRDIPKSNLLGDDGHVKIADFGVSNQF 300
QY 301 EGNDQALSSTAGTAPFAPEAISDSGQSFSGKALDVMATGVTLYCFVYKGPFFIDDFILA 360
DB 301 EGNDQALSSTAGTAPFAPEAISDSGQSFSGKALDVMATGVTLYCFVYKGPFFIDDFILA 360
QY 361 LHRKIKNEPVVPEPPEISEELKDLILKMLDKNPETRIGVDPDKLHPWVTNKGPEPLPSE 420
DB 361 LHRKIKNEPVVPEPPEISEELKDLILKMLDKNPETRIGVDPDKLHPWVTNKGPEPLPSE 420
QY 421 EEHCSSVETSEEVKNSVRLIPSWTTLVLSMLKRSFGNPFEPQARREERSMAGNL 480
DB 421 EEHCSSVETSEEVKNSVRLIPSWTTLVLSMLKRSFGNPFEPQARREERSMAGNL 480
QY 481 LVKEGFGEGKSPPELPGVQ 499
DB 481 LVKEGFGEGKSPPELPGVQ 499

Db 481 LVKEGFGEGKSPPELPGVQ 499
RESULT 8
US-10-092-900A-58
1 Sequence 58, Application US/10092900A
2 Publication No. US20040043382A1
3 GENERAL INFORMATION:
4 APPLICANT: Padigar, Muralidhara
5 APPLICANT: Spytek, Kimberly A.
6 APPLICANT: Shenoy, Suresh G.
7 APPLICANT: Taupier Jr., Raymond J.
8 APPLICANT: Pena, Carol E.A.
9 APPLICANT: Li, Li
10 APPLICANT: Zerhusen, Bryan D.
11 APPLICANT: Gusev, Vladimir Y.
12 APPLICANT: Ji, Weizhen
13 APPLICANT: Gorman, Linda
14 APPLICANT: Miller, Charles E.
15 APPLICANT: Kekuda, Ramesh
16 APPLICANT: Patturajan, Meera
17 APPLICANT: Gangolli, Esha A.
18 APPLICANT: Vernet, Corine A.M.
19 APPLICANT: Guo, Xiaojia Sasha
20 APPLICANT: Tchernev, Velizar T.
21 APPLICANT: Fernandes, Elma R.
22 APPLICANT: Casman, Stacie J.
23 APPLICANT: Malyankar, Uriel M.
24 APPLICANT: Gerlach, Valerie
25 APPLICANT: Liu, Yi
26 APPLICANT: Anderson, David W.
27 APPLICANT: Spaderma, Steven K.
28 APPLICANT: Catterton, Elina
29 APPLICANT: Leite, Mario W.
30 APPLICANT: Zhong, Haihong
31 APPLICANT: Alsobrook, John P.
32 APPLICANT: Lepley, Denise M.
33 APPLICANT: Rieger, Daniel K.
34 APPLICANT: Burgess, Catherine E.
35 TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
36 FILE REFERENCE: 21402-290C
37 CURRENT APPLICATION NUMBER: US/10/092,900A
38 CURRENT FILING DATE: 2002-03-07
39 PRIOR APPLICATION NUMBER: USSN 60/274,322
40 PRIOR FILING DATE: 2001-03-08
41 PRIOR APPLICATION NUMBER: USSN 60/283,675
42 PRIOR FILING DATE: 2001-04-13
43 PRIOR APPLICATION NUMBER: USSN 60/338,092
44 PRIOR FILING DATE: 2001-12-03
45 PRIOR APPLICATION NUMBER: USSN 60/274,281
46 PRIOR FILING DATE: 2001-03-08
47 PRIOR APPLICATION NUMBER: USSN 60/274,191
48 PRIOR FILING DATE: 2001-03-08
49 PRIOR APPLICATION NUMBER: USSN 60/325,681
50 PRIOR FILING DATE: 2001-09-27
51 PRIOR APPLICATION NUMBER: USSN 60/304,354
52 PRIOR FILING DATE: 2001-07-10
53 PRIOR APPLICATION NUMBER: USSN 60/279,995
54 PRIOR FILING DATE: 2001-03-30
55 PRIOR APPLICATION NUMBER: USSN 60/294,899
56 PRIOR FILING DATE: 2001-05-31
57 PRIOR APPLICATION NUMBER: USSN 60/287,424
58 Remaining Prior Application data removed - See File Wrapper or PALM.
59 NUMBER OF SEQ ID NOS: 768
60 SEQ ID NO 58
61 LENGTH: 543
62 TYPE: PRT
63 ORGANISM: Homo sapiens
64 US-10-092-900A-58

Query Match 98.1%; Score 2585; DB 12; Length 543;
Best Local Similarity 92.4%; Pred. No. 5.7e-201;

Matches 502; Conservative 0; Mismatches 3; Indels 38; Gaps 1;
Qy 1 MEGGPAVCCDPRAELVERVAADVTHLEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60
Db 1 MEGGPAVCCDPRAELVERVAADVTHLEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60
Qy 61 LLPARPSLSARKLSQRPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
Db 61 LLPARPSLSARKLSQRPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
Qy 121 DCVOLNOYKQSEIGKAGYGVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRPGSQ 180
Db 121 DCVOLNOYKQSEIGKAGYGVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRPGSQ 180
Qy 181 AAQGGPAKQLPLERVYQETAILKKLDHNVNVKLIIEVLDPAEDNLVLAQNQAQNTQLD 240
Db 181 AAQGGPAKQLPLERVYQETAILKKLDHNVNVKLIIEVLDPAEDNLVLAQNQAQNTQLD 240
Qy 229 -----VFDLLRKGPVMEVPCDKPFSEQARLYLRDVILG 262
Db 241 STNIAKSHLLPSQQSGSTWAARSVFDLLRKGPVMEVPCDKPFSEQARLYLRDVILG 300
Qy 263 LEYLHCQKIVHRDIKPSNLLIGDDGHVKIADFGVSNQFEGNDAQLSSTAGTAPFMAPEAI 322
Db 301 LEYLHCQKIVHRDIKPSNLLIGDDGHVKIADFGVSNQFEGNDAQLSSTAGTAPFMAPEAI 360
Qy 323 SDSQSFSGKALDWATGVTLYCFVYKCPPIIDFIALHKKIKNEPVVPEEPEISEEL 382
Db 361 SDSQSFSGKALDWATGVTLYCFVYKCPPIIDFIALHKKIKNEPVVPEEPEISEEL 420
Qy 383 KDLILKMLDKNPETRIGVPDIKLPWTKNGEERHCSVVEVTEGEVKNSVRLIP 442
Db 421 KDLILKMLDKNPETRIGVPDIKLPWTKNGEERHCSVVEVTEGEVKNSVRLIP 480
Qy 443 SWTTVILVKMLRKSRFCGNPPEQARREERSMSPAGNLLVKEGFGEGKSPELFGVQDE 502
Db 481 SWTTVILVKMLRKSRFCGNPPEQARREERSMSPAGNLLVKEGFGEGKSPELFGVQDE 540
Qy 503 AAS 505
Db 541 AAS 543

RESULT 9
US-10-092-900A-54
; Sequence 54, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina

; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 54
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-54

Query Match 97.2%; Score 2560; DB 12; Length 503;
Best Local Similarity 98.2%; Pred. No. 5.4e-199;
Matches 496; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

Qy 1 MEGGPAVCCDPRAELVERVAADVTHLEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60
Db 1 MEGGPAVCCDPRAELVERVAADVTHLEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60
Qy 61 LLPARPSLSARKLSQRPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
Db 61 LLPARPSLSARKLSQRPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
Qy 121 DCVOLNOYKQSEIGKAGYGVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRPGSQ 180
Db 121 DCVOLNOYKQSEIGKAGYGVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRPGSQ 180
Qy 181 AAQGGPAKQLPLERVYQETAILKKLDHNVNVKLIIEVLDPAEDNLVLAQNQAQNTQLD 240
Db 181 AAQGGPAKQLPLERVYQETAILKKLDHNVNVKLIIEVLDPAEDNLVLAQNQAQNTQLD 240
Qy 241 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLIGDDGHVKIADFGVSNQF 300
Db 240 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLIGDDGHVKIADFGVSNQF 299
Qy 301 EGNDQAQLSSTAGTAPFMAPEAISDSGQSFSGK-LDVWATGVTLYCFVYKCPPIIDFILA 360
Db 300 EGNDQAQLSSTAGTAPFMAPEAISDSGQSFSGK-LDVWATGVTLYCFVYKCPPIIDFILA 358
Qy 361 LHRKIKNEPVVPEEPEISEELKOLILKMLDKNPETRIGVPDIKLPWTKNGEPELSE 420
Db 359 LHRKIKNEPVVPEEPEISEELKOLILKMLDKNPETRIGVPDIKLPWTKNGEPELSE 418
Qy 421 EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKMLRKSRFCGNPPEQARREERSMSPAGNLL 480
Db 419 EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKMLRKSRFCGNPPEQARREERSMSPAGNLL 478

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QY 481 LVKEGFGGKSPELPGVQDEAAS 505
Db 479 LVKEGFGGKSPELPGVQDEAAS 503

RESULT 10
US-10-135-689-4
; Sequence 4, Application US/10135689
; Publication No. US20020123121A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000904DIV II
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-135-689-4

Query Match 93.7%; Score 2468; DB 13; Length 505;
Best Local Similarity 93.5%; Pred. No. 1.6e-191;
Matches 472; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPPPRARAASVIPGSTR 60
Db 1 MERSPAVCCQDPRAELVERVAISVAHLEAEAGPEPASNGVDPPPRARAASVIPGASR 60

QY 61 LIPAPSLSARKLSQERPAAGVYLAQAGPYATGPASHISPRAWRPTTIESHHVAISDAE 120
Db 61 PTPVPSLSARKFSQERPAAGVYLAQAGPYATGPASHISPRAWRPTTIESHHVAISDTE 120

QY 121 DCVQLNOYKLOEIGKAGVGVRLAYNESEDHRYAMKVLKKLLKQYGFPRPPRGSQ 180
Db 121 DCVQLNOYKLOEIGKAGVGVRLAYNEREDHRYAMKVLKKLLKQYGFPRPPRGSQ 180

QY 181 AAQGGPAKOLLPLERVYQEIAILKKLDHVVNVVKLIEVLDPAEDNLVYVFDLLRKGPMVE 240
Db 181 APQGGPAKOLLPLERVYQEIAILKKLDHVVNVVKLIEVLDPAEDNLVYVFDLLRKGPMVE 240

QY 241 VPCDKPFSEQARLYLRDVLGLEYLHCOKI VHRDIKPSNLLGGDGHVKIADFGVSNQF 300
Db 241 VPCDKPFSEQARLYLRDVLGLEYLHCOKI VHRDIKPSNLLGGDGHVKIADFGVSNQF 300

QY 301 EGNDAQLSSTAGTAPFMAPEAISDGSQSFSGKALDVWATGVTLYCFVYKCPFIIDFILA 360
Db 301 EGNDAQLSSTAGTAPFMAPEAISDGSQSFSGKALDVWATGVTLYCFVYKCPFIIDFILA 360

QY 361 LHRKIKNEAVVPFPEPVESEELKDLILKMLDKNPETRIGVPIKLPWTKNGEPLPSE 420
Db 361 LHRKIKNEAVVPFPEPVESEELKDLILKMLDKNPETRIGVPIKLPWTKNGEPLPSE 420

QY 421 EHCSEVVEVTEGEVKNVSLIPSWTTVILVKMLAKRSFGNPFEPQARREERMSAPGNL 480
Db 421 EHCSEVVEVTEGEVKNVSLIPSWTTVILVKMLAKRSFGNPFEPQARREERMSAPGNL 480

QY 481 LVKEGFGGKSPELPGVQDEAAS 505
Db 481 LVKEGFGGKSPELPGVQDEAAS 505

RESULT 11
US-10-690-617-4
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; Sequence 4, Application US/10690617
; Publication No. US20040086926A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000904DIV II
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-690-617-4

Query Match 93.7%; Score 2468; DB 16; Length 505;
Best Local Similarity 93.5%; Pred. No. 1.6e-191;
Matches 472; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPPPRARAASVIPGSTR 60
Db 1 MERSPAVCCQDPRAELVERVAISVAHLEAEAGPEPASNGVDPPPRARAASVIPGASR 60

QY 61 LIPAPSLSARKLSQERPAAGVYLAQAGPYATGPASHISPRAWRPTTIESHHVAISDAE 120
Db 61 PTPVPSLSARKFSQERPAAGVYLAQAGPYATGPASHISPRAWRPTTIESHHVAISDTE 120

QY 121 DCVQLNOYKLOEIGKAGVGVRLAYNESEDHRYAMKVLKKLLKQYGFPRPPRGSQ 180
Db 121 DCVQLNOYKLOEIGKAGVGVRLAYNEREDHRYAMKVLKKLLKQYGFPRPPRGSQ 180

QY 181 AAQGGPAKOLLPLERVYQEIAILKKLDHVVNVVKLIEVLDPAEDNLVYVFDLLRKGPMVE 240
Db 181 APQGGPAKOLLPLERVYQEIAILKKLDHVVNVVKLIEVLDPAEDNLVYVFDLLRKGPMVE 240

QY 241 VPCDKPFSEQARLYLRDVLGLEYLHCOKI VHRDIKPSNLLGGDGHVKIADFGVSNQF 300
Db 241 VPCDKPFSEQARLYLRDVLGLEYLHCOKI VHRDIKPSNLLGGDGHVKIADFGVSNQF 300

QY 301 EGNDAQLSSTAGTAPFMAPEAISDGSQSFSGKALDVWATGVTLYCFVYKCPFIIDFILA 360
Db 301 EGNDAQLSSTAGTAPFMAPEAISDGSQSFSGKALDVWATGVTLYCFVYKCPFIIDFILA 360

QY 361 LHRKIKNEAVVPFPEPVESEELKDLILKMLDKNPETRIGVPIKLPWTKNGEPLPSE 420
Db 361 LHRKIKNEAVVPFPEPVESEELKDLILKMLDKNPETRIGVPIKLPWTKNGEPLPSE 420

QY 421 EHCSEVVEVTEGEVKNVSLIPSWTTVILVKMLAKRSFGNPFEPQARREERMSAPGNL 480
Db 421 EHCSEVVEVTEGEVKNVSLIPSWTTVILVKMLAKRSFGNPFEPQARREERMSAPGNL 480

QY 481 LVKEGFGGKSPELPGVQDEAAS 505
Db 481 LVKEGFGGKSPELPGVQDEAAS 505

RESULT 12
US-10-205-823-52
; Sequence 52, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
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; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-52
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```
Query Match 57.9%; Score 1525.5; DB 14; Length 556;
Best Local Similarity 62.0%; Pred. No. 5.5e-115; Indels 31; Gaps 5;
Matches 299; Conservative 77; Mismatches 75;

Qy 30 EADGGPEPTRNGVDPPPPARAASVPGSTSLRLPARELSARKLSLOER-----PAGSYL 84
Db 75 EADQGEVP-----LDSSGSQ---ARPHLSGRKLSLQERSQGGLAAGGSL 115

Qy 85 EAQAG-----PYATGPASHISPRAMRRPTIESHHVAISDAEDCVQLNOYKLOSEIGKA 138
Db 116 DMNGRCICPSLPYSPVSSPQSSPRLPRPTVESHHVSIITGMQDCVQLNQYTLKDEIGKGS 175

Qy 139 YGVVRLAYNESEDRHYAMKVLKSKLLKQYGFPRPPRPGSGAAQGGPAKQLLPLERVYQ 198
Db 176 YGVVRLAYNENDNTYAMKVLKSKLLKQYGFPRPPRPGSGAAQGGPAKQLLPLERVYQ 235

Qy 199 EAILKXLDHVNKKLIEVLDDPAEDNLVYFDLLRKGPMVEVPCDKPFSEEARLYLRD 258
Db 236 EAILKXLDHNPVKKLIEVLDDPNEDHLYMVFEVNLQGVNMFVTLKPLSEDAQRFYQD 295

Qy 259 VILGLEVYHCKIVHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDAQLSSTAGTAPMA 318
Db 296 LIKGIEYHYQKIITHRDIKPSNLLVGDGHGHIKIADFGVSNFEGKSDALLSNTVGTAPMA 355

Qy 319 PEALSDSGSQSGKALDVWATGVTLYCFVYKCPFFIDDFILALHRKIKNEPVPWPEPEI 378
Db 356 PESLSETRKIFSGKALDVWANGVTLYCFVQCFPMDBERIMCLHSKLSQALEFPDQDI 415

Qy 379 SEELKDLILKMLDKNPETRIQVDPDKLHPWVTKNGEPLPSEEBHCSVVEVTEGEVNSV 438
Db 416 AEDLKDLITRMLDKNPESRIWVPEIKLHPWVTRHGAEPLPSEDENCITLVEVTEBEVNSV 475

Qy 439 RLIPSWTIVILVKMLRKRSGNPFEPQARREERSMSPAGNLLVKEGEGKSPPLPGV 498
Db 476 KHIPSLATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSLXGT 534

Qy 499 QE 500
Db 535 KK 536
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RESULT 13
US-10-316-124-9
```

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; Sequence 9, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: WPI01-291P1RM
; CURRENT APPLICATION NUMBER: US/10/316,124
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-316-124-9

Query Match 57.6%; Score 1518.5; DB 14; Length 588;
Best Local Similarity 63.3%; Pred. No. 2.2e-114; Indels 31; Gaps 5;
Matches 295; Conservative 75; Mismatches 65;

Qy 30 EADGGPEPTRNGVDPPPPARAASVPGSTSLRLPARELSARKLSLOER-----PAGSYL 84
Db 75 EADQGEVP-----LDSSGSQ---ARPHLSGRKLSLQERSQGGLAAGGSL 115

Qy 85 EAQAG-----PYATGPASHISPRAMRRPTIESHHVAISDAEDCVQLNOYKLOSEIGKA 138
Db 116 DMNGRCICPSLPYSPVSSPQSSPRLPRPTVESHHVSIITGMQDCVQLNQYTLKDEIGKGS 175

Qy 139 YGVVRLAYNESEDRHYAMKVLKSKLLKQYGFPRPPRPGSGAAQGGPAKQLLPLERVYQ 198
Db 176 YGVVRLAYNENDNTYAMKVLKSKLLKQYGFPRPPRPGSGAAQGGPAKQLLPLERVYQ 235

Qy 199 EAILKXLDHVNKKLIEVLDDPAEDNLVYFDLLRKGPMVEVPCDKPFSEEARLYLRD 258
Db 236 EAILKXLDHNPVKKLIEVLDDPNEDHLYMVFEVNLQGVNMFVTLKPLSEDAQRFYQD 295

Qy 259 VILGLEVYHCKIVHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDAQLSSTAGTAPMA 318
Db 296 LIKGIEYHYQKIITHRDIKPSNLLVGDGHGHIKIADFGVSNFEGKSDALLSNTVGTAPMA 355

Qy 319 PEALSDSGSQSGKALDVWATGVTLYCFVYKCPFFIDDFILALHRKIKNEPVPWPEPEI 378
Db 356 PESLSETRKIFSGKALDVWANGVTLYCFVQCFPMDBERIMCLHSKLSQALEFPDQDI 415

Qy 379 SEELKDLILKMLDKNPETRIQVDPDKLHPWVTKNGEPLPSEEBHCSVVEVTEGEVNSV 438
Db 416 AEDLKDLITRMLDKNPESRIWVPEIKLHPWVTRHGAEPLPSEDENCITLVEVTEBEVNSV 475

Qy 439 RLIPSWTIVILVKMLRKRSGNPFEPQARREERSMSPAGNLLVKE 484
Db 476 KHIPSLATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKK 520

RESULT 14
US-10-295-027-1355
; Sequence 1355, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
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; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1355
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1355
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Query Match      57.6%; Score 1518.5; DB 15; Length 588;
Best Local Similarity 63.3%; Pred. No. 2.2e-114;
Matches 295; Conservative 75; Mismatches 65; Indels 31; Gaps 5;

QY 30 EADGGPEPTRNGVDPPTPRARAASVTPGTSRLLPARPSLSARKLSIQER-----PAGSYL 84
DB 75 EADGGPEPTRNGVDPPTPRARAASVTPGTSRLLPARPSLSARKLSIQER-----PAGSYL 84
QY 85 EAQAG-----PYATGPASHISPRAWRRPTTISHHVAISDAEDCVOLNQYKLGSGKGA 138
DB 116 DMNGRCICPSLPSYSPVSSQSSPRLPRPTVSHSHVSIITGMQDCVOLNQYTLKDEIGKGS 175
QY 139 YGVWKLAYNESDRHYAMKVLKSKKLLKQYGFPRPPRPGSQAAQGGPAKQLPLERVYQ 198
DB 176 YGVWKLAYNENDTYAMKVLKSKKLLKQAGFPFRPPRGTTPAGGCIQPRGPIEQVYQ 235
QY 199 EIALKLDHNVVVKLIEVLDPAEDNLYLVFDLLRKGPVMEVPCDKPFSEEQARLYLRD 258
DB 236 EIALKLDHNVVVKLIEVLDPAEDNLYLVFDLLRKGPVMEVPCDKPFSEEQARLYLRD 258
QY 259 VILGLEYLHCOKI VHRDIKPSNLLIGDDGHVKIADFGVSNQEPGNDALSSTAGTPAFMA 318
DB 296 LKGEYLYHYQKLIHRDIKPSNLLIGDDGHVKIADFGVSNQEPGNDALSSTAGTPAFMA 355
QY 319 PEATSDSQSGSKALDVMATGTYLCFYVYKCPFDIDFIALHRKIKNEPVVFPPEEPEI 378
DB 356 PESLSETRKIFSGKALDVMATGTYLCFYVYKCPFDIDFIALHRKIKNEPVVFPPEEPEI 378
QY 379 SEELKDLILKMDKNPETRIGVDPDKLHPWTKNGEELPSEEEHCSVVVEVTEGVKNSV 438
DB 416 AEDLKDLITRMLDKNPESRIVVPEIKLHPWTRHGAELPLPSDENCTLVETEVEEVNSV 475
QY 439 RLIPSTWTVILVKSMRKESFGNPPQARRREERSMSAPGNLLVKE 484
DB 476 KHIPSLATVILVKTMIRKRSFGNPPQARRREERSMSAPGNLLVKE 520
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RESULT 15
US-10-205-823-54
; Sequence 54, Application US/10205823
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; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wansley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumel
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-54
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Query Match      55.9%; Score 1472.5; DB 14; Length 417;
Best Local Similarity 68.9%; Pred. No. 7.4e-111;
Matches 272; Conservative 72; Mismatches 50; Indels 1; Gaps 1;

QY 90 PYATGPASHISPRAWRRPTTISHHVAISDAEDCVOLNQYKLGSGKGA 149
DB 11 PYSVPSSQSSPRLPRPTVSHSHVSIITGMQDCVOLNQYTLKDEIGKGSYGVWKLAYNEN 70
QY 150 EDRHYAMKVLKSKKLLKQYGFPRPPRPGSQAAQGGPAKQLPLERVYQETAILKLDHVP 209
DB 71 DNTYAMKVLKSKKLLKQAGFPFRPPRGTTPAGGCIQPRGPIEQVYQETAILKLDHVP 130
QY 210 NVVKLIEVLDPAEDNLYLVFDLLRKGPVMEVPCDKPFSEEQARLYLRD 269
DB 131 NVVKLIEVLDPAEDNLYLVFDLLRKGPVMEVPCDKPFSEEQARLYLRD 190
QY 270 KIVHRDIKPSNLLIGDDGHVKIADFGVSNQEPGNDALSSTAGTPAFMAPEAISQSGSF 329
DB 191 KIIHRDIKPSNLLIGDDGHVKIADFGVSNQEPGNDALSSTAGTPAFMAPEAISQSGSF 250
QY 330 SGKALDVMATGTYLCFYVYKCPFDIDFIALHRKIKNEPVVFPPEEPEI 389
DB 251 SGKALDVMATGTYLCFYVYKCPFDIDFIALHRKIKNEPVVFPPEEPEI 310
QY 390 LDKNPETRIGVDPDKLHPWTKNGEELPSEEEHCSVVVEVTEGVKNSV 449
DB 311 LDKNPESRIVVPEIKLHPWTRHGAELPLPSDENCTLVETEVEEVNSV 370
QY 450 VKSMRKESFGNPPQARRREERSMSAPGNLLVKE 484
DB 371 VKTMIRKESFGNPPQARRREERSMSAPGNLLVKE 404
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Search completed: July 12, 2004, 05:55:51
Job time : 1697 secs
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